

111023

Ruhl, Mary Jane

From: Schnizer, Holly
Sent: Monday, December 29, 2003 10:29 AM
To: STIC-Biotech/ChemLib
Subject: seq. search for appl. no. 09/809,827

emp# 76558

Please search all databases (inc. interference) for SEQ ID NO: 31 and rev. translation of SEQ ID NO:31.

Thank you.

Holly Schnizer
AU 1653
CM1-9E09
305-3722
mailbox: CM1-9B01

*PLEASE SCAN
SUMMARY of SEARCH*

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:51:25 ; Search time 17 Seconds
(without alignments)
821.584 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 1553

Sequence: 1 MGDHAWSLKFLAGAVAAA.....LRGMGAFVLVLYDEIKYV 297

Scoring table: BLOSUM62

Gapop 10.0., Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526.5	98.3	298	1	ADT1_HUMAN
2	1466.5	94.4	298	1	ADT1_RAT
3	1463.5	94.2	298	1	ADT1_MOUSE
4	1453.5	93.6	297	1	ADT1_BOVIN
5	1408.5	90.7	298	1	ADT2_MOUSE
6	1407.5	90.6	298	1	ADT2_RAT
7	1398.5	90.1	298	1	ADT2_HUMAN
8	1385.5	89.2	298	1	ADT3_HUMAN
9	1380.5	88.9	298	1	ADT3_BOVIN
10	1241	79.9	299	1	ADT1_DROME
11	1162.5	74.9	301	1	ADT1_ANOGA
12	973.5	62.7	339	1	ADT1_CHLKE
13	770.5	49.6	308	1	ADT1_CHLRE
14	756.5	48.7	387	1	ADT1_MAIZE
15	752.5	48.5	322	1	ADT1_SCHPO
16	752.5	48.5	386	1	ADT1_GOSHI
17	751.5	48.4	382	1	ADT1_ORYZA
18	751.5	48.4	387	1	ADT2_MAIZE
19	746	48.0	381	1	ADT1_ARATH
20	744.5	47.9	386	1	ADT1_SOLTU
21	742.5	47.8	331	1	ADT1_WHEAT
22	740	47.6	386	1	ADT1_SOLTU
23	736	47.4	307	1	ADT3_YEAST
24	734	47.3	318	1	ADT2_YEAST
25	733.5	47.2	313	1	ADT1_NEUCR
26	731	47.1	385	1	ADT2_ARATH
27	729	46.9	305	1	ADT1_KLULA
28	728.5	46.9	331	1	ADT2_WHEAT
29	716.5	46.3	309	1	ADT1_YEAST
30	702.5	19.5	678	1	CNC1_HUMAN
31	300.5	19.3	330	1	GDC_BOVIN
32	296.5	19.1	565	1	CNC3_CABEL
33	296.5	19.1	702	1	CNC1_CABEL

RESULT 1

ID	ADT1_HUMAN	STANDARD;	PRT;	298 AA.
AC	P12235;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	ADP, ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).			
GN	SLC25A4 OR ANT1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
EN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89236396; PubMed=2541251;			
RA	Cozens A.L., Runswick M.J., Walker J.E.;			
RT	"DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";			
RL	J. Mol. Biol. 206:261-280 (1989).			
EN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89340499; PubMed=2547778;			
RA	Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,			
RA	Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;			
RT	"A human muscle adenine nucleotide translocator gene has four exons, is located on chromosome 4, and is differentially expressed.";			
RL	J. Biol. Chem. 264:13988-14004 (1989).			
EN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88041149; PubMed=2823266;			
RA	Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;			
RT	"cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584 (1987).			
EN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Whiting J., Halton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			

34	296	19.1	588	1	CNC2_CABEL
35	295	19.0	322	1	GDC_RAT
36	292.5	18.8	307	1	ODC3_YEAST
37	292	18.8	332	1	GDC_HUMAN
38	291	18.7	675	1	CNC2_HUMAN
39	280	18.0	315	1	MPT_HUMAN
40	279.5	18.0	676	1	CNC2_MOUSE
41	270.5	17.4	315	1	SAL8_HUMAN
42	267.5	17.2	325	1	UCP5_MOUSE
43	266.5	17.2	310	1	ODC3_YEAST
44	265.5	17.1	325	1	UCP5_HUMAN
45	263.5	17.0	695	1	CNC1_DROME

ALIGNMENTS

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RA Butterfield V.S.N., Krywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RN SEQUENCE OF 1-37 FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=88124845; PubMed=2829183;
RX Houldsworth J., Attardi G.;
RA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
level in adult human liver.";
Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
[6]
RN VARIANTS: PEO PRO-114 AND MET-289.
RP MEDLINE=20385067; PubMed=10926541;
RX Kaukonen J., Juselius J.K., Tiranti V., Kytala A., Zeviani M.,
RA Comi G.P., Keranen J., Peltonen L., Suomalainen A.;
RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
Science 289:782-785(2000).
RL Science 289:782-785(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant
progressive external ophthalmoplegia with various mitochondrial
DNA deletions (PEO). Patients with PEO have mitochondrial
myopathy, progressive external ophthalmoplegia, and other
abnormalities associated with multiple different deletions of
mitochondrial DNA.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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or send an email to license@sib-sib.ch).

DR EMBL; J02966; AAA61223.1; -;
DR EMBL; J03593; AAA36751.1; -;
DR EMBL; J04982; AAA51736.1; -;
DR EMBL; BC008664; AA086664.1; -;
DR PIR; A44778; A44778.
DR Genbank; HGNC:10990; SLC25A4.
DR MIM; 103220; -;
DR MIM; 157640; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005739; C:mitochondrion; TAS.
DR GO; GO:0015207; F:adenine transporter activity; TAS.
DR GO; GO:0006091; P:energy pathways; TAS.
DR GO; GO:0000002; P:mitochondrial genome maintenance; TAS.
DR GO; GO:0006832; P:small molecule transport; TAS.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
multigene family; Disease mutation.
DR TRANSMEM 12 29
DR TRANSMEM 73 91 1 (POTENTIAL).
DR TRANSMEM 117 134 2 (POTENTIAL).
DR TRANSMEM 176 195 4 (POTENTIAL).
DR TRANSMEM 214 231 5 (POTENTIAL).
DR TRANSMEM 273 291 6 (POTENTIAL).
DR TRANSMEM 1 110 1.
DR TRANSMEM 111 208 2.

FT REPEAT 209 298 3.
FT VARIANT 114 114 A -> P (IN PEO).
FT FTID=VAR_012111.
FT V -> M (IN PEO).
FT VARIANT 289 289 /FTID=VAR_012112.
FT FTID=VAR_012112.
FT CONFLICT 16 16 G -> A (IN REF. 3).
FT CONFLICT 147 149 KGA -> RR (IN REF. 3).
FT CONFLICT 227 227 V -> L (IN REF. 3).
SQ SEQUENCE 298 AA; 33064 MW; 59F0DFAC4E7CFBB CRC64;
Query Match 98.3%; Score 1526.5; DB 1; Length 298;
Best Local Similarity 98.3%; Pred. No. 28-129;
Matches 293; Conservative 2; Mismatches 1; Gaps 1;
QY 1 MGDHAWSLKDFLAGAAVAASKTAVAPIERVKLLLOVHASKQISAEQYKGIIDCVVR 60
DB 1 MGDHAWSLKDFLAGAAVAASKTAVAPIERVKLLLOVHASKQISAEQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-PAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-PAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180
QY 180 VQGIIRYRAAYFGVDTAKGMLPDPKQNVHIFYSWMTAQSVTAVAGLLSYPFDTVRRMM 239
DB 181 VQGIIRYRAAYFGVDTAKGMLPDPKQNVHIFYSWMTAQSVTAVAGLLSYPFDTVRRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAPVLVLYDEIKKYV 297
DB 241 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAPVLVLYDEIKKYV 298
RESULT 2
ADTI RAT
ID ADT1 RAT STANDARD; PRT; 298 AA.
AC Q05962;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinohara Y., Kamida M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
EXTENT, IN BRAIN AND KIDNEY.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:51:25 ; Search time 17 seconds
(without alignments)
821.584 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 1553

Sequence: 1 MGDHWSFLKFLAGAVAAA.....LRGMGAFVLVLYDEIKYV 297

Scoring table: BLOSUM62

Gapop 10.0., Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126.5	98.3	298	1 ADT1_HUMAN	P12235 homo sapien
2	146.5	94.4	298	1 ADT1_RAT	Q05962 rattus norv
3	1463.5	94.2	298	1 ADT1_MOUSE	P48962 mus musculu
4	1453.5	93.6	297	1 ADT1_BOVIN	P02722 bos taurus
5	1408.5	90.7	298	1 ADT2_MOUSE	P51881 mus musculu
6	1407.5	90.6	298	1 ADT2_RAT	Q09073 rattus norv
7	1398.5	90.1	298	1 ADT2_HUMAN	P05141 homo sapien
8	1385.5	89.2	298	1 ADT3_HUMAN	P12236 homo sapien
9	1380.5	88.9	298	1 ADT3_BOVIN	P32007 bos taurus
10	1241.5	79.9	299	1 ADT1_DROME	*Q26365 drosophila
11	1162.5	74.9	301	1 ADT_ANGOA	*Q27238 anopheles g
12	973.5	62.7	339	1 ADT_CHLXE	P31692 chlorella k
13	770.5	49.6	308	1 ADT_CHLRE	P07080 chlamydomon
14	756.5	48.7	387	1 ADT1_MAIZE	P04709 zea mays (m
15	752.5	48.5	322	1 ADT1_SCHPO	Q09188 schizosacch
16	752.5	48.5	386	1 ADT1_GOSHI	Q22342 gossypium h
17	751.5	48.4	382	1 ADT_ORYSA	P31691 oryza sativ
18	751.5	48.4	387	1 ADT2_MAIZE	P12857 zea mays (m
19	746	48.0	381	1 ADT1_ARATH	P31167 arabidopsis
20	744.5	47.9	386	1 ADT1_SOLTU	P25083 solanum tub
21	742.5	47.8	331	1 ADT1_WHEAT	P41629 triticum ae
22	740	47.6	386	1 ADT2_SOLTU	P27081 solanum tub
23	736	47.4	307	1 ADT3_YEAST	P18238 saccharomyc
24	734	47.3	318	1 ADT2_YEAST	P18239 saccharomyc
25	733.5	47.2	313	1 ADT_NEUCR	P02723 neurospora
26	731	47.1	385	1 ADT2_ARATH	P40941 arabidopsis
27	729	46.9	305	1 ADT1_KLULA	P49382 kluyveromyc
28	728.5	46.9	331	1 ADT2_WHEAT	Q41630 triticum ae
29	718.5	46.3	309	1 ADT1_YEAST	P04710 saccharomyc
30	302.5	19.5	678	1 CMC1_HUMAN	O07146 homo sapien
31	300.5	19.3	330	1 GDC_BOVIN	Q01888-bos-taurus
32	296.5	19.1	565	1 CMC3_CABEL	Q19529 caenorhabdi
33	296.5	19.1	702	1 CMC1_CABEL	Q21153 caenorhabdi

RESULT 1
ADT1_HUMAN
ID ADT1_HUMAN STANDARD; PRT; 298 AA.
AC P12235;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocator 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANTI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89340499; PubMed=2547778;
RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J., Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
RT "A human muscle adenine nucleotide translocator gene has four exons, is located on chromosome 4, and is differentially expressed.";
RL J. Biol. Chem. 264:13928-14004(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88041149; PubMed=2823266;
RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=EYE;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.P., Bhat N.K., Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Heieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

ALIGNMENTS

34 296 19.1 588 1 CMC2_CABEL
35 295 19.0 322 1 GDC_RAT
36 292.5 18.8 307 1 ODC2_YEAST
37 292 18.8 332 1 GDC_HUMAN
38 291 18.7 675 1 CMC2_HUMAN
39 280 18.0 315 1 MFT_HUMAN
40 279.5 18.0 676 1 CMC2_MOUSE
41 270.5 17.4 315 1 SAI18_HUMAN
42 267.5 17.2 325 1 UCP5_MOUSE
43 266.5 17.2 310 1 ODC1_YEAST
44 265.5 17.1 325 1 UCP5_HUMAN
45 263.5 17.0 695 1 CMC1_DROME

Q20799 caenorhabdi
P16261 rattus norv
Q99297 saccharomyc
P16260 homo sapien
Q94980 homo sapien
Q94981 homo sapien
Q94982 mus musculu
Q94983 mus musculu
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RN SEQUENCE OF 1-37 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 RN [6]
 RP VARIANTS: PEO PRO-114 AND MET-289.
 RX MEDLINE=20385067; PubMed=10926541;
 RA Kaukonen J., Juselius J.K., Tiranti V., Kytala A., Zeviani M.,
 RA Comi G.P., Keranen J., Peltonen L., Suomalainen A.;
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
 RL Science 289:782-785(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant
 CC progressive external ophthalmoplegia with various mitochondrial
 CC DNA deletions (PEO). Patients with PEO have mitochondrial
 CC myopathy, progressive external ophthalmoplegia, and other
 CC abnormalities associated with multiple different deletions of
 CC mitochondrial DNA.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR ENBL; J02966; AAA61223.1; -;
 DR ENBL; J03593; AAA36751.1; -;
 DR ENBL; J04982; AAA51735.1; -;
 DR ENBL; BC008664; AAH08664.1; -;
 DR PIR; A44778; A44778.
 DR Genew; HGNC:10990; SLC25A4.
 DR MIM; 103220; -;
 DR MIM; 157640; -;
 DR CO; GO:0005887; C:integral to plasma membrane; TAS.
 DR CO; GO:0005739; C:mitochondrion; TAS.
 DR CO; GO:0015207; P:adenine transporter activity; TAS.
 DR CO; GO:0006091; P:energy pathways; TAS.
 DR CO; GO:0000002; P:mitochondrial genome maintenance; TAS.
 DR CO; GO:0006832; P:small molecule transport; TAS.
 DR InterPro; IPR002067; Mit carrier.
 DR InterPro; IPR002030; Mit uncoupling.
 DR InterPro; IPR001993; Mitoch carrier.
 DR Pfam; PF00153; mito carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family; Disease mutation.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.

FT REPEAT 209 298 3.
 FT VARIANT 114 114 A -> P (IN PEO).
 FT /FTID=VAR 012111.
 FT V -> M (IN PEO).
 FT VARIANT 289 289 /FTID=VAR 012112.
 FT CONFLICT 16 16 G -> A (IN REF. 3).
 FT CONFLICT 147 149 KGA -> RR (IN REF. 3).
 FT CONFLICT 227 227 V -> L (IN REF. 3).
 SQ SEQUENCE 298 AA; 33064 MW; 59F0DFARC4E7CFBB CRC64;
 Query Match 98.3%; Score 1526.5; DB 1; Length 298;
 Best Local Similarity 98.3%; Pred. No. 28-129;
 Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
 QY 1 MGDHWSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKQISAQYKGIIDCVVR 60
 DB 1 MGDHWSFLKDFLAGGAAVASKTAVAPIERVKLLLOVHASKQISAQYKGIIDCVVR 60
 QY 61 IPKEQGFISFWGNLANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
 DB 61 IPKEQGFISFWGNLANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTLAADYGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNV 179
 DB 121 GAAGATSLCFVYPLDFARTLAADYGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNV 180
 QY 180 VQGIIRYRAAYGVVDYTAGMPLDPKQNVHIFVSWIAQSVTAVAGLLSPFDTVRRMM 239
 DB 181 VQGIIRYRAAYGVVDYTAGMPLDPKQNVHIFVSWIAQSVTAVAGLLSPFDTVRRMM 240
 QY 240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFPGANVLRGMGGAFVLVLYDEIKYV 297
 DB 241 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFPGANVLRGMGGAFVLVLYDEIKYV 298
 RESULT 2
 ADT1 RAT
 ID ADT1 RAT STANDARD; PRT; 298 AA.
 AC Q05962;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP.ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 DE translocase 1) (adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANT1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinohara Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
 CC EXTENT, IN BRAIN AND KIDNEY.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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DR EMBL; X61667; CAA43842.1; -.
DR EMBL; D12770; BAA02237.1; -.
DR PIR; I60173; I60173.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32989 MW; 66704FP78C5BC320 CRC64;

Query Match          94.4%; Score 1466.5; DB 1; Length 298;
Best Local Similarity 94.3%; Pred. No. 4.7e-124;
Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDFLAGAAVASTVAPISRVKLLQVHQAQISAEKQYKGIICVVR 60
DB 1 MGDQALSFLKDFLAGGAAVASTVAPISRVKLLQVHQAQISAEKQYKGIICVVR 60
QY 61 IPKEQGLSFWRGNLNVIYFTQALNPAFKDKYKQLFLGGVDRHKQFVYFAGNLASG 120
DB 61 IPKEQGLSFWRGNLNVIYFTQALNPAFKDKYKQLFLGGVDRHKQFVYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGRKQSFQREFNGLDCLTKIFKSDGLRGLYQGFNVS 180
QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKRVHIFVSNMIAQSVTAVAGLLSYFPDVRMM 239
DB 181 VQGIILYRAAYFGVYDTAKGMLPDPKRVHIFVSNMIAQSVTAVAGLLSYFPDVRMM 240
QY 240 QSGRKADIMYTGTCVDCWRKIADDEGAKAPFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
DB 241 QSGRKADIMYTGTCVDCWRKIADDEGAKAPFKGAWSNVLRGMGGAFVLVLYDEIKKYV 298

RESULT 3
ADT1_MOUSE STANDARD; PRT; 298 AA.
AC P48962; Q62164;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE ADP-ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (mANCI1).
GN SLC25A4 OR ANT1 OR ANCI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudoautosomal genes and their mouse
RL homologs."
RM Mamm. Genome 7:25-30 (1996).
[2]

RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Muscle;
RA Laplace C., Costet P.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
RT translocase 1 and 2 genes."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -I- SUBUNIT: Homodimer.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -I- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U27315; AAC52837.1; -.
DR EMBL; X74510; CAA52616.1; -.
DR EMBL; AF240002; AAF64470.1; -.
DR EMBL; BC003791; AAH03791.1; -.
DR EMBL; BC026925; AAH26925.1; -.
DR PIR; S37210; S37210.
DR MGD; MGI:1353495; Slc25a4.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.

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FT REPEAT      111 208 2.
FT REPEAT      209 298 3.
FT CONFLICT    136 136 F -> L (IN REF. 1).
SQ SEQUENCE     298 AA; 32904 MW; 3A849FEAB09B1462 CRC64;

Query Match      94.2%; Score 1463.5; DB 1; Length 298;
Best Local Similarity 94.0%; Pred. No. 8.7e-124;
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAATAVAVKTAAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
DB 1 MGDQALSFLKDFLAGGTAATAVAVKTAAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
QY 61 IPKEQGLSWRGNLANVIRVFTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASG 120
DB 61 IPKEQGLSWRGNLANVIRVFTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNV 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNV 180
QY 180 VQGIIRYRAAYFGVYDTAKGMLPDPKPNVHIIVSWMIAQSVTAVAGLLSYFPDTRRRMM 239
DB 181 VQGIIRYRAAYFGVYDTAKGMLPDPKPNVHIIVSWMIAQSVTAVAGLLSYFPDTRRRMM 240
QY 240 QSGRKGADIMYTGTCVDCWRKIADKGAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
DB 241 QSGRKGADIMYTGTCVDCWRKIADKGAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 298

RESULT 4
ADT1_BOVIN
ID ADT1_BOVIN STANDARD; PRT; 297 AA.
AC P02722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP, ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1)
DE (Adenine nucleotide translocator 1) (ANT 1).
GN SLC2A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873 (1989).
RN [2]
RP SEQUENCE.
RX MEDLINE=82188267; PubMed=7076130;
RA Aquila H., Misra D., Bulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349 (1982).
RN [3]
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=86295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence.";
RL Biochem. Biophys. Res. Commun. 138:850-857 (1986).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.

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EMBL; M13783; AAA30363.1; -
EMBL; M24102; AAA30768.1; -
PIR; A43646; XWBO.
InterPro; IPR002067; Mit carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
Multigene family; Methylation.
INIT_MET 0 0
MOD_RES 1 1 1
FT MOD_RES 51 51 1
FT TRANSMEM 11 28 1
FT TRANSMEM 72 90 2
FT TRANSMEM 116 133 3
FT TRANSMEM 175 194 4
FT TRANSMEM 213 230 5
FT TRANSMEM 272 290 6
FT REPEAT 1 110 1
FT REPEAT 111 207 2
FT REPEAT 208 297 3
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AEB48 CRC64;

Query Match      93.6%; Score 1453.5; DB 1; Length 297;
Best Local Similarity 94.6%; Pred. No. 6.8e-123;
Matches 280; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 3 DHWSFLKDFLAGAATAVAVKTAAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIP 62
DB 2 DQALSFLKDFLAGGTAATAVAVKTAAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIP 61
QY 63 KEQGLSWRGNLANVIRVFTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASGA 122
DB 62 KEQGLSWRGNLANVIRVFTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASGA 121
QY 123 AGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQ 181
DB 122 AGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQ 181
QY 182 GIIIRYRAAYFGVYDTAKGMLPDPKPNVHIIVSWMIAQSVTAVAGLLSYFPDTRRRMMQ 241
DB 182 GIIIRYRAAYFGVYDTAKGMLPDPKPNVHIIVSWMIAQSVTAVAGLLSYFPDTRRRMMQ 241
QY 242 GSKGADIMYTGTCVDCWRKIADKGAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
DB 242 GSKGADIMYTGTCVDCWRKIADKGAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297

RESULT 5
ADT2_MOUSE
ID ADT2_MOUSE STANDARD; PRT; 298 AA.
AC P51881; Q61311;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP, ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

```

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; Tissue=Brain;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 homologs."; Mamm. Genome 7:25-30(1996).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP Tissue=Skeletal muscle;
 RC Sheldon J.G.;
 RA Thesis (1995), University of Cambridge, U.K.
 RL [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Costet P., Laplace C.;
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RA Laplace C.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20432087; PubMed=10974536;
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 translocase 1 and 2 genes."; Gene 254:57-66(2000).
 RL [6]
 CC -f- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -i- SUBUNIT: Homodimer.
 CC -i- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -i- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -i- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC [1]
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR ENBL; U27316; AAC52838.1; --
 DR ENBL; U10404; AAA19009.1; --
 DR ENBL; X70847; CAA50196.1; --
 DR ENBL; AF240003; AAF64471.1; --
 DR MGD; MGI:1353496; SLC25a5.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT REPEAT 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;
 SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;
 Query Match 90.7%; Score 1408.5; DB 1; Length 298;
 Best Local Similarity 89.6%; Pred. No. 7.3e-119;

Matches 266; Conservative 17; Mismatches 13; Indels 1; Gaps 1;
 QY 1 MGDHAWSLKDLFAGAVAAVSKTAVAPIERVKLLQVQASHQKSAEQYKGIIDCVVR 60
 DB 1 MTDAVSPAKDFLAGGVAARIKSTAVAPIERVKLLQVQASHQKSAEQYKGIIDCVVR 60
 QY 61 IPKEQGLSFWRGNLNVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
 DB 61 IPKEQGLSFWRGNLNVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPARTLAADVGR--AOREPHGLGDCIIKPKSGDLGLYQGFNV 179
 DB 121 GAAGATSLCFVYPLDPARTLAADVGR--AOREPHGLGDCIIKPKSGDLGLYQGFNV 180
 QY 180 VQIIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSLSPFDVRRMM 239
 DB 181 VQIIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSLSPFDVRRMM 240
 QY 240 QSGRGADIMYGTGTCWRKIAKDEGAKAPFKGANSNVLGRMGGAFLVLYDIKKY 296
 DB 241 QSGRGADIMYGTGTCWRKIAKDEGAKAPFKGANSNVLGRMGGAFLVLYDIKKY 297
 RESULT 6
 ADT2_RAT STANDARD; PRT; 298 AA.
 ID ADT2_RAT
 AC Q09073;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; Tissue=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinohara Y., Kamada M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 encoding rat mitochondrial adenine nucleotide translocator."; Biochim. Biophys. Acta 1152:192-196(1993).
 RL [1]
 CC -i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -i- SUBUNIT: Homodimer.
 CC -i- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -i- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC -i- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -i- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC [1]
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR ENBL; D12771; BAA02238.1; --
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.

```

FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EF35 CRC64;

Query Match 90.6%; Score 1407.5; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 9e-119;
Matches 266; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGVAASVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
Db 1 MTDAAVSPAKDFLAGGVAASISKTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60

QY 61 IPKEQGLSPWRGNLANVIRYFTQALNPAFKDKYKQLFLGGVDHKKQFWRYFAGNLSG 120
Db 61 IPKEQGLSPWRGNLANVIRYFTQALNPAFKDKYKQLFLGGVDHKKQFWRYFAGNLSG 120

QY 121 GAAGATSLCPVPLDFARTLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
Db 121 GAAGATSLCPVPLDFARTLAADVGKAGAREFEKGLGDCIVKIKYKSDGKGLYQGFNVS 180

QY 180 VQGIILYRAAYFGYDTAKMLPDPKKNVHIFVSWMTAQSVTAAGLLSYFPDTPVRMM 239
Db 181 VQGIILYRAAYFGYDTAKMLPDPKKNVHIFISWMTAQSVTAAGLLSYFPDTPVRMM 240

QY 240 QSGRKGADIMYTGDCWRKIADEGAKAPFKGWSNVLKGMGAFVLYLDEIKY 296
Db 241 QSGRKGADIMYTGDCWRKIADEGAKAPFKGWSNVLKGMGAFVLYLDEIKY 297

RESULT 7
ID ADT2 HUMAN STANDARD; PRT; 298 AA.
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP, ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence."
RL J. Biol. Chem. 265:16060-16063 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated."
RL J. Biol. Chem. 262:4355-4358 (1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R.,
RA Mazzarella R.A., Schlusser D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.

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RA Becker M., Graves T., Ozersky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M57424; AAA51737.1; -
DR EMBL; J02683; AAA35579.1; -
DR EMBL; L78810; AAB39286.1; -
DR EMBL; AC004000; AAB96347.1; -
DR EMBL; J03591; AAA36749.1; -
DR PIR; A29132; A29132.
DR Genew; HGNC:10991; SLC25A5.
DR MIM; 300150; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0015207; F:adenine transporter activity; TAS.
DR GO; GO:0006832; P:small molecule transport; TAS.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 6 6 V -> L (IN REF. 2).
FT CONFLICT 66 66 R -> E (IN REF. 2).
FT CONFLICT 111 111 G -> L (IN REF. 4 AND 5).
FT CONFLICT 162 162 V -> G (IN REF. 5).
SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 90.1%; Score 1398.5; DB 1; Length 298;
Best Local Similarity 88.1%; Pred. No. 5.8e-118;
Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGVAASVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
Db 1 MTDAAVSPAKDFLAGGVAASISKTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60

QY 61 IPKEQGLSPWRGNLANVIRYFTQALNPAFKDKYKQLFLGGVDHKKQFWRYFAGNLSG 120
Db 61 IPKEQGLSPWRGNLANVIRYFTQALNPAFKDKYKQLFLGGVDHKKQFWRYFAGNLSG 120

```

QY 121 GAAGATSLCPVYPLDFAITRLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
 DB 121 GAAGATSLCFVYPLDFAITRLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180
 QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSVTAVAGLLSYPPDFTVRRMM 239
 DB 181 VQGIILYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSVTAVAGLLSYPPDFTVRRMM 240
 QY 240 QSGRKGADIMYTGTVDCWRKIADEGAKAFKFGANVLRGMGAFVLYLDEIKKY 296
 DB 241 QSGRKGADIMYTGTVDCWRKIADEGAKAFKFGANVLRGMGAFVLYLDEIKKY 297

RESULT 8
 ADT3 HUMAN
 ID ADT3 HUMAN STANDARD; PRT; 298 AA.
 AC P1236; Q96C49;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
 DE (Adenine nucleotide translocator 3) (ANT 3).
 GN SLC25A6 OR ANT3
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89236396; PubMed=2541251;
 RA Copens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 RT ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280 (1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhou J., Yu W., Tang H., Mei G., Teang Y.T.M., Bouck J., Gibbs R.A.,
 RA Margolin J.F.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Cervix, Eye, and Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S., Krzywinska M.I., Skalska U., Smallus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE OF 36-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).
 CC -|- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.

CC -|- SUBUNIT: Homodimer.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -|- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -|- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC -----
 CC EMBL; J03592; AAA36750.1; -;
 CC EMBL; AY007135; AAG01998.1; -;
 CC EMBL; BC007295; AAH07295.1; -;
 CC EMBL; BC007850; AAH07850.1; -;
 CC EMBL; BC008737; AAH08737.1; -;
 CC EMBL; BC008935; AAH08935.1; -;
 CC EMBL; BC014775; AAH14775.1; -;
 CC FIR; S03894; S03894.
 CC Genew; HGNC:10992; SLC25A6.
 CC MIM; 300151; -;
 CC MIM; 403000; -;
 CC GO; GO:0005744; C:mitochondrial inner membrane translocase co. .; TAS.
 CC GO; GO:0005471; P:ATP/ADP antiporter activity; NAS.
 CC GO; GO:006854; P:ATP/ADP exchange; TAS.
 CC InterPro; IPR002067; Mit_carrier.
 CC InterPro; IPR002030; Mit_uncoupling.
 CC InterPro; IPR001993; Mitoch_carrier.
 CC Pfam; PF00153; mito_car; 3.
 CC PRINTS; PR00926; MITOCARRIER.
 CC PRINTS; PR00784; MTUNCOUPLING.
 CC PROSITE; PS00215; MITOCH_CARRIER; 3.
 CC KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 100 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 105 108 KHTQ -> RHA (IN REF. 4).
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
 SQ SEQUENCE 298 AA; 32866 MW; 18534E9F0B49672F CRC64;
 Query Match 89.2%; Score 1385.5; DB 1; Length 298;
 Best Local Similarity 87.2%; Pred. No. 8.4e-117;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MGDHAWSLFKDLAGAAVAAVSKTAVAPIERVKLLQVHASKQISAERQYKGIIDCVVR 60
 DB 1 MTEQAISFAKDFLAGIAAAISKTAVAPIERVKLLQVHASKQIAADQYKGIIDCVR 60
 QY 61 IPKEQGLSFRGNLANVIRYPTQALNPAFKDKYKQLFLGVDVDRHKQFWRYFAGNLAG 120
 DB 61 IPKEQGLSFRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKHTQFWRYFAGNLAG 120
 QY 121 GAAGATSLCFVYPLDFAITRLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
 DB 121 GAAGATSLCFVYPLDFAITRLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180
 QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSVTAVAGLLSYPPDFTVRRMM 239
 DB 181 VQGIILYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSVTAVAGLLSYPPDFTVRRMM 240
 QY 240 QSGRKGADIMYTGTVDCWRKIADEGAKAFKFGANVLRGMGAFVLYLDEIKKY 297
 DB 241 QSGRKGADIMYTGTVDCWRKIADEGAKAFKFGANVLRGMGAFVLYLDEIKKY 298

FT TRANSMEM 178 197 4 (POTENTIAL).
FT TRANSMEM 216 233 5 (POTENTIAL).
FT TRANSMEM 275 293 6 (POTENTIAL).
SQ SEQUENCE 301 AA; 32863 MW; 4CC9E17C9F8DA08B CRC64;

Query Match 74.9%; Score 1162.5; DB 1; Length 301;
Best Local Similarity 76.9%; Pred. No. 7.9e-97;
Matches 223; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 6 WSLFKPLAGAVAAVSKTAVPIERVKLLQVQHASKOISAEKQYKGIIDCVVRIPKEQ 65
DB 8 YGFAKPLAGISAAVSKTAVPIERVKLLQVQHASKOISAEKQYKGIIDCVVRIPKEQ 67

QY 66 GFLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKGFWRYFAGNLASGGAAGA 125
DB 68 GIGAFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKGFWRYFAGNLASGGAAGA 127

QY 126 TSLCFVYPLDFARTLAADVGRRA-QREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGI 184
DB 128 TSLCFVYPLDFARTLAADVGRRA-QREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGI 187

QY 185 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSYPPDTVRRRMMQSGR 244
DB 188 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSYPPDTVRRRMMQSGR 247

QY 245 GADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGGAFVLVLYDEIK 294
DB 248 KSEVMYKNTLDCWKIKQEGSGGAFKGAWSNVLRGMGGAFVLVLYDEIK 297

RESULT 12
ADT CHLKE STANDARD; PRT; 339 AA.
ID ADT CHLKE
AC P31592;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
OS Chlorella kessleri.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3074;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92084708; PubMed=1748677;
RA Hilgarth C., Sauer N., Tanner W.;
RT "Glucose increases the expression of the ATP/ADP translocator and the glyceroldehyde-3-phosphate dehydrogenase genes in Chlorella.";
RL J. Biol. Chem. 266:24044-24047(1991).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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CC
CC EMBL; M76669; AAA33027.1; -.
DR PIR; A41677; A41677.
DR InterPro; IPR002067; Mit carrier.
DR ProDom; PRD00193; Mitoch carrier.
DR Pfam; PF00153; mito carr; 3.
DR PRINTS; PS00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 45 62 1 (POTENTIAL).
FT TRANSMEM 108 126 2 (POTENTIAL).
FT TRANSMEM 151 168 3 (POTENTIAL).
FT TRANSMEM 209 228 4 (POTENTIAL).
FT TRANSMEM 248 265 5 (POTENTIAL).
FT TRANSMEM 304 322 6 (POTENTIAL).
SQ SEQUENCE 339 AA; 36686 MW; 54779734A33B942 CRC64;

Query Match 62.7%; Score 973.5; DB 1; Length 339;
Best Local Similarity 65.3%; Pred. No. 7.6e-80;
Matches 192; Conservative 30; Mismatches 65; Indels 7; Gaps 4;

QY 7 SFLKPLAGAVAAVSKTAVPIERVKLLQVQHASKOISAEKQYKGIIDCVVRIPKE 64
DB 40 AFVKLLAGTATAGTATAVPIERVKLLQVQHASKOISAEKQYKGIIDCVVRIPKE 99

QY 65 QGFLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKGFWRYFAGNLASGGAAGA 124
DB 100 QGVASFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKGFWRYFAGNLASGGAAGA 158

QY 125 ATSLCFVYPLDFARTLAADVGRRA-QREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGI 184
DB 159 AGSLTIVYPLDFARTLAADVGRRA-QREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGI 218

QY 185 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSYPPDTVRRRMMQSGR 243
DB 219 VTRGAYFGVYDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSYPPDTVRRRMMQSGR 276

QY 244 KGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGGAFVLVLYDEIKYV 297
DB 277 -GGERQYNGTIDCWRRKVAQEGMKAFKGAWSNVLRGMGGAFVLVLYDEIKYV 329

RESULT 13
ADT CHLRE STANDARD; PRT; 308 AA.
ID ADT CHLRE
AC P27080;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
GN ABT.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FUD44-R2;
RX MEDLINE=93204887; PubMed=8455552;
RA Sharpe J.A., Day A.;
RT "Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtii.";
RL Mol. Gen. Genet. 237:134-144(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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CC
CC EMBL; X65194; CAA46311.1; -.

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CC 294 --KKY 296
 Db 378 FGKY 382

RESULT 15
 ADT_SCHPO STANDARD; PRT; 322 AA.
 AC Q09188;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADP ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
 DE translocator) (ANT).
 GN ANCI OR SPBC530.10C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=96257204; PubMed=8675018;
 RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide
 RT carrier of Schizosaccharomycetes pombe by functional complementation in
 RT Saccharomycetes cerevisiae.";
 RL Gene 171:113-117(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., William R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moulé S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Sesger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voicakert G., Aert R., Robben J., Grymonprez B.,
 RA Waltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.I., Moreno S., Armstrong J., Forsburg S.L.,
 RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Sipakovski G.V., Ussery D., Barréll B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomycetes pombe.";
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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Query Match 48.5%; Score 752.5; DB 1; Length 322;
 Best Local Similarity 52.9%; Pred. NO. 4.4e-60;
 Matches 156; Conservative 51; Mismatches 75; Indels 13; Gaps 6;
 QY 7 SFLKDFLAGAATAAAYSKTAVPIRVKLLLOVQHASKQISAEEK---QYKGIIDCVVRIPK 63
 Db 26 TFFDFPMGGSAAVSKTAAPIRVKLLIQN---DEMIRAGRLSHRYKIGECFKRTAA 83
 QY 64 EQGFLSFWRGNLAVIRYPTQALNFAFKDKYKQLFLGGVDRHFKQFWRFYAGNLASGGAA 123
 Db 84 EGVISLWNGTANVIRYPTQALNFAFKDKYKQLFLGGVDRHFKQF---GYKKERDGYAKWFAAGNLASGGAA 142
 QY 124 GATSLCFVYPLDFARTLAAD---VGRRAQRFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
 Db 143 GAASLLFVYSLDYARTLANDAKSAKKGGERQFNGLVVDVYRTYRSGLRGLYRGFGPSV 202
 QY 181 QGIIIVRAAYFGVYDTAKG-MLPDPKQNVHIFVSWIAQSVTAVAGLLSYPPFTVRRMMW 239
 Db 203 VGIVVYRGVLYFGMDTLKPVVILVGLPNEGFLASFLLGWAVTTGSGVASVPLDITIRRRMM 262
 QY 240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAPVLVLYDEIK 294
 Db 263 TSGEA---VKYSSSFEQGRQILAKEGARSFFKAGANILRGVAGAGVLSIYDQVQ 314

Search completed: December 30, 2003, 09:55:04
 Job time : 18 secs

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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:51:26 ; Search time 41 Seconds
(without alignments)
1869.308 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 1553

Sequence: 1 MGDHWSFLKDFLAGAVAAA.....LRMGGAFLVLYDIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virius:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1464.5	94.3	298	6 O46373	O46373 oryctolagus
2	1462.5	94.2	298	11 Q8BV19	Q8BV19 mus musculus
3	1411.5	90.9	298	6 Q8SQH5	Q8SQH5 bos taurus
4	1392.5	89.7	298	13 Q8AYM3	Q8AYM3 gallus gall
5	1377.5	88.7	298	13 Q9VIC4	Q9VIC4 rana rugosa
6	1377.5	88.7	298	13 Q9PRH1	Q9PRH1 rana rugosa
7	1375.5	88.6	298	13 Q8JH10	Q8JH10 brachydontio
8	1374.5	88.5	298	13 Q9PRH2	Q9PRH2 rana rugosa
9	1366.5	88.0	298	13 Q919M9	Q919M9 xenopus lae
10	1245.5	80.2	299	5 Q95YX4	Q95YX4 ethomstigm
11	1241.5	79.9	300	5 Q9NHW5	Q9NHW5 lucilia cup
12	1241.5	79.9	312	5 Q8IRA0	Q8IRA0 drosophila
13	1234.5	79.5	317	13 Q91336	Q91336 rana sylvat
14	1183	76.2	288	5 O44094	O44094 drosophila
15	1183	76.2	288	5 O44093	O44093 drosophila
16	1180.5	76.0	254	11 Q8BKQ5	Q8BKQ5 mus musculus

17	1147	73.9	307	5	O62526	O62526 drosophila
18	1139.5	73.4	304	5	Q25129	Q25129 halocynthia
19	1101.5	70.9	315	4	Q9H0C2	Q9H0C2 homo sapien
20	1045.5	67.3	313	5	P91410	P91410 caenorhabdi
21	1043.5	67.2	313	5	Q21103	Q21103 caenorhabdi
22	1042	67.1	310	10	Q8H727	Q8H727 phytophthor
23	1037.5	66.8	300	5	O45865	O45865 caenorhabdi
24	1005.5	64.7	300	5	O01813	O01813 caenorhabdi
25	993.5	64.0	300	5	Q17407	Q17407 caenorhabdi
26	989.5	63.7	309	5	Q97470	Q97470 dictyosteli
27	959	61.8	307	8	Q9XM22	Q9XM22 ascaris suu
28	950	61.2	307	8	Q9BJ36	Q9BJ36 toxoplasma
29	926.5	59.7	301	5	Q8MV4	Q8MV4 euploies ep
30	916.5	59.0	308	5	Q8MVR8	Q8MVR8 nycototherus
31	914.5	58.9	305	5	Q8MVR7	Q8MVR7 nycototherus
32	913.5	58.8	306	5	Q8MVR5	Q8MVR5 nycototherus
33	908.5	58.5	301	5	Q81J34	Q81J34 plasmodium
34	906.5	58.4	308	5	Q8MVR6	Q8MVR6 nycototherus
35	904.5	58.3	301	5	Q25692	Q25692 plasmodium
36	904.5	58.3	301	5	Q25692	Q25692 plasmodium
37	841.5	54.2	170	6	Q9XS69	Q9XS69 sus scrofa
38	772	49.7	306	5	Q18683	Q18683 caenorhabdi
39	757.5	48.8	305	3	Q9P8M1	Q9P8M1 varrowia li
40	750.5	48.3	307	5	O76286	O76286 trypanosoma
41	748.5	48.2	303	3	O74260	O74260 candida par
42	746.5	48.1	379	10	O49447	O49447 arabidopsis
43	745.5	48.0	326	5	P91270	P91270 caenorhabdi
44	743.5	47.9	307	5	Q26697	Q26697 trypanosoma
45	743	47.8	302	3	Q8J0M2	Q8J0M2 varrowia li

ALIGNMENTS

RESULT 1

O46373	ID	O46373	PRELIMINARY;	PRT;	298 AA.
AC	O46373;				
DT	01-JUN-1998 (TREMBLrel. 06, Created)				
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	ADP/ATP translocase.				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX	NCBI_TaxID=9986;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Skeletal muscle;				
RA	Yamaguchi N., Kasai M.;				
RT	"Identification of a 30kDa calsequestrin-binding protein, which				
RT	regulates calcium release from sarcoplasmic reticulum of rabbit				
RT	skeletal muscle.";				
RL	J. Biochem. 335:541-547 (1998).				
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.				
DR	EMBL; AB009386; BAA23777.1; -				
DR	InterPro: IPR001993; Mitoch carrier.				
DR	InterPro: IPR002067; Mit carrier.				
DR	PIfam; PF00153; mito_carr; 3.				
DR	PRINTS; PR00926; MITOCARRIER.				
DR	PRINTS; PR00784; MTUNCOUPLING.				
DR	PROSITE; PS00215; MITOCH CARRIER; 3.				
KW	Membrane; Transmembrane; Transport.				
SQ	SEQUENCE 298 AA; 32901 MW; CAA32C88164AD78 CRC64;				

Query Match 94.3%; Score 1464.5; DB 6; Length 298;
Best Local Similarity 94.6%; Pred. No. 7.2e-129;
Matches 282; Conservative 8; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAVAAA...KTAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60

DB 1 MSDQALSFLKDFLAGGVA...KTAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60

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QY 61 IPKEQGLSFWRGNLNVIRYPTQALNFAFKDKYKOLFGLGGVDRHKQFWRYPAGNLSG 120
DE |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OS |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_
RP SEQUENCE FROM N.A.
RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
RT "structural properties of mammalian mitochondrial ADP/ATP carriers:
RT identification of possible amino acids that determine functional
RT differences in its isoforms.";
RL Mitochondrion 1:371-379(2002).
DR EMBL; AB065433; BAB84673.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;

RESULT 2
Q8BV19 PRELIMINARY; PRT; 298 AA.
AC Q8BV19
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Solute carrier family 25.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK078077; BAC37117.1; -.
SQ SEQUENCE 298 AA; 32904 MW; F94C89009836710B CRC64;

Query Match 94.2%; Score 1462.5; DB 11; Length 298;
Best Local Similarity 94.0%; Pred. No. 1.1e-128;
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAATAVSKTAVPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
DB 1 MGDKALSFLKDFLAGGTAATAVSKTAVPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNVIRYPTQALNFAFKDKYKOLFGLGGVDRHKQFWRYPAGNLSG 120
DB 61 IPKEQGLSFWRGNLNVIRYPTQALNFAFKDKYKOLFGLGGVDRHKQFWRYPAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
QY 180 VQGIITRYAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 239
DB 180 VQGIITRYAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 239
QY 240 QSGRKADIMYTGTVDCWRKIADKGAFAFFKGAWSNVLKRGMGAFVLVLYDEIKKYV 297
DB 241 QSGRKADIMYTGTVDCWRKIADKGAFAFFKGAWSNVLKRGMGAFVLVLYDEIKKYV 298

RESULT 3
Q8SQH5 PRELIMINARY; PRT; 298 AA.
AC Q8SQH5
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Solute carrier family 25.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK078077; BAC37117.1; -.
SQ SEQUENCE 298 AA; 32904 MW; F94C89009836710B CRC64;

Query Match 94.2%; Score 1462.5; DB 11; Length 298;
Best Local Similarity 94.0%; Pred. No. 1.1e-128;
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAATAVSKTAVPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
DB 1 MGDKALSFLKDFLAGGTAATAVSKTAVPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNVIRYPTQALNFAFKDKYKOLFGLGGVDRHKQFWRYPAGNLSG 120
DB 61 IPKEQGLSFWRGNLNVIRYPTQALNFAFKDKYKOLFGLGGVDRHKQFWRYPAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
QY 180 VQGIITRYAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 239
DB 180 VQGIITRYAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 239
QY 240 QSGRKADIMYTGTVDCWRKIADKGAFAFFKGAWSNVLKRGMGAFVLVLYDEIKKYV 297
DB 241 QSGRKADIMYTGTVDCWRKIADKGAFAFFKGAWSNVLKRGMGAFVLVLYDEIKKYV 298

RESULT 4
Q8AYM3 PRELIMINARY; PRT; 298 AA.
AC Q8AYM3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ATP/ADP antiporter.
GN AVANT.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;
RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP
RT and ANT mRNA in chicken skeletal muscle.";
RL FEBS Lett. 0:0-0(2002).
DR EMBL; AB088686; BAC15533.1; -.
SQ SEQUENCE 298 AA; 32847 MW; 1174CC5EC400A10D CRC64;

Query Match 89.7%; Score 1392.5; DB 13; Length 298;
Best Local Similarity 88.3%; Pred. No. 4e-122;
Matches 263; Conservative 18; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAATAVSKTAVPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60

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Db 1 MADQATSLKDFLARGVAAAIKSTAVAPIERVLKLLQVHASKQIAADKQYKGIIDCVVR 60
QY 61 IPKEQGFSLFWRGNLANVIRYPTQALNPAFKDKYKQFLGGVDHKKQFWRYPAGNLASG 120
Db 61 IPKEQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQVFLGGVDKHTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR - AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
Db 121 GAAGATSLCFVYPLDFARTLAADVGR - AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180
QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDVTVRMM 239
Db 181 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDVTVRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGGAFLVLYDIKYYV 297
Db 241 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGGAFLVLYDIKYYV 298

RESULT 5
QYIC4 PRELIMINARY; PRT; 298 AA.
ID QYIC4
AC QYIC4;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Winkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008457; BAA36507.1; -
DR EMBL; AB008456; BAA36506.1; -
DR EMBL; AB008461; BAA36511.1; -
DR EMBL; AB008462; BAA36512.1; -
DR InterPro; IPR001993; Mitoch. carrier.
DR InterPro; IPR002067; Mit. carrier.
DR InterPro; IPR002030; Mit. uncoupling.
DR Pfam; PF00153; mito carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH. CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 88.7%; Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%; Pred. No. 1e-120;
Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHAWSLKDFLAGVAAAVKSTAVAPIERVLKLLQVHASKQIAADKQYKGIIDCVVR 60
Db 1 MTDAAISFAKDFLAGGVAIAIKSTAVAPIERVLKLLQVHASKQITADKQYKGIIDCVVR 60
QY 61 IPKEQGFSLFWRGNLANVIRYPTQALNPAFKDKYKQFLGGVDHKKQFWRYPAGNLASG 120
Db 61 IPKEQGFVSWRGNLANVIRYPTQALNPAFKDKYKIFLDNVDKRTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR - AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
Db 121 GAAGATSLCFVYPLDFARTLAADVGR - AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180
QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDVTVRMM 239
Db 181 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDVTVRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGGAFLVLYDIKYYV 297
Db 241 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGGAFLVLYDIKYYV 298

RESULT 7
QYIC4 PRELIMINARY; PRT; 298 AA.
ID QYIC4
AC QYIC4;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Solute carrier family 25 member 5 protein.
GN SLC25A5.
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Db 241 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGGAFLVLYDIKYYV 298
QYIC4 PRELIMINARY; PRT; 298 AA.
ID QYIC4
AC QYIC4;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Winkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008463; BAA36513.1; -
DR EMBL; AB008456; BAA36506.1; -
DR EMBL; AB008461; BAA36511.1; -
DR EMBL; AB008462; BAA36512.1; -
DR InterPro; IPR001993; Mitoch. carrier.
DR InterPro; IPR002067; Mit. carrier.
DR InterPro; IPR002030; Mit. uncoupling.
DR Pfam; PF00153; mito carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH. CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match 88.7%; Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%; Pred. No. 1e-120;
Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHAWSLKDFLAGVAAAVKSTAVAPIERVLKLLQVHASKQIAADKQYKGIIDCVVR 60
Db 1 MTDAAISFAKDFLAGGVAIAIKSTAVAPIERVLKLLQVHASKQITADKQYKGIIDCVVR 60
QY 61 IPKEQGFSLFWRGNLANVIRYPTQALNPAFKDKYKQFLGGVDHKKQFWRYPAGNLASG 120
Db 61 IPKEQGFVSWRGNLANVIRYPTQALNPAFKDKYKIFLDNVDKRTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR - AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
Db 121 GAAGATSLCFVYPLDFARTLAADVGR - AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180
QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDVTVRMM 239
Db 181 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDVTVRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGGAFLVLYDIKYYV 297
Db 241 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGGAFLVLYDIKYYV 298

RESULT 7
QYIC4 PRELIMINARY; PRT; 298 AA.
ID QYIC4
AC QYIC4;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Solute carrier family 25 member 5 protein.
GN SLC25A5.
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Db 1 MTDAAISFAKDFLAGGVAASIKTAVAPIERVKLLQVQHASKOITADKHKGIMDCVVR 60
QY 61 IPKEQGLFSLFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDHRKHQFWRYPAGNLASG 120
Db 61 IPKEQGLFSLFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDHRKHQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGRRA-ORFPHGLGDCIIFIKPSDGLRGLYQGFNV 179
Db 121 GAAGATSLCFVYPLDFARTLAADVGRRA-ORFPHGLGDCIIFIKPSDGLRGLYQGFNV 180
QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSUTAVAGLLSYPPDTRRRMM 239
Db 181 VQGIILYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSUTAVAGLLSYPPDTRRRMM 240
QY 240 QSGRKGADIMYTGTCWRKRIADDEGAKAFPKGAWSNVLRGMGAFVLVLYDEIKKYV 297
Db 241 QSGRKGADIMYTGTCWRKRIADDEGAKAFPKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 10
Q95VX4 PRELIMINARY; PRT; 299 AA.
AC Q95VX4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE ADP-ATP translocator.
OS Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
OX NCBI_TaxID=62613;
RN 1;
RP SEQUENCE FROM N.A.
RA Burnell J.N.;
RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus rubripes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401758; AAL02100.1;
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carri_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
DR MEMBRANE; Transmembrane; Transport.
SQ SEQUENCE 299 AA; 33037 MW; 3C3BBCB26E7C3C5E CRC64;

Query Match 80.28; Score 1245.5; DB 5; Length 299;
Best Local Similarity 80.3%; Pred. No. 2.3e-108;
Matches 236; Conservative 25; Mismatches 32; Indels 1; Gaps 1;

QY 5 AWSFLKDFLAGVAAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRIKPE 64
Db 5 AWSFLKDFLAGVAAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRIKPE 64
QY 65 QGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDHRKHQFWRYPAGNLASGAAG 124
Db 65 QGILSYWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDHRKHQFWRYPAGNLASGAAG 124
QY 125 ATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIFIKPSDGLRGLYQGFNV 183
Db 125 ATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIFIKPSDGLRGLYQGFNV 184
QY 184 IYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSUTAVAGLLSYPPDTRRRMMQSGR 243
Db 185 IYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSUTAVAGLLSYPPDTRRRMMQSGR 244
QY 244 KGADIMYTGTCWRKRIADDEGAKAFPKGAWSNVLRGMGAFVLVLYDEIKKYV 297
Db 245 KKADILYKNTIDCWGKIYKTEGGAAPFKGAFSNILRGTGGAFLVLVLYDEIKALI 298

RESULT 11
Q9NHWS PRELIMINARY; PRT; 300 AA.
ID Q9NHWS

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AC Q9NHWS;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=SS mal seeking;
RA Chen Z., Fair J.A., Batterham P.;
RT "A cDNA clone encoding the ADP/ATP translocase of Lucilia cuprina."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF218587; AAF32322.1;
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carri_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
DR MEMBRANE; Transmembrane; Transport.
SQ SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;

Query Match 79.9%; Score 1241.5; DB 5; Length 300;
Best Local Similarity 78.7%; Pred. No. 5.6e-108;
Matches 236; Conservative 25; Mismatches 36; Indels 3; Gaps 1;

QY 1 MGDHAAA--WSFLKDFLAGVAAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDC 57
Db 1 MGDHAAA--WSFLKDFLAGVAAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDC 60
QY 58 VVRIPKEQGLFSLFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDHRKHQFWRYPAGNL 117
Db 61 FVRIPKEQGLFSLFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDHRKHQFWRYPAGNL 120
QY 118 ASGGAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIFIKPSDGLRGLYQGFN 177
Db 121 ASGGAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIFIKPSDGLRGLYQGFN 180
QY 178 VSVQGIILYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSUTAVAGLLSYPPDTRRRM 237
Db 181 VSVQGIILYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSUTAVAGLLSYPPDTRRRM 240
QY 238 MQSGRKGADIMYTGTCWRKRIADDEGAKAFPKGAWSNVLRGMGAFVLVLYDEIKKYV 297
Db 241 MQSGRKGADIMYTGTCWRKRIADDEGAKAFPKGAWSNVLRGMGAFVLVLYDEIKKYV 300

RESULT 12
Q8IRA0 PRELIMINARY; PRT; 312 AA.
ID Q8IRA0;
AC Q8IRA0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG16944-PC.
GN SESB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1;
RP SEQUENCE FROM N.A.
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H., Blazej R.G., Champe M., Pfeiffer B.D.,

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Db 121 GAAGATSLCFVYPLDFARTLAAADVAGKAGAGREFNGLGDCCLAKIFKSDGLKGLYQGFNVS 180
QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSYPPDVTVRMM 239
Db 181 VQGIILYRAAYFGIYDTAKGMLPDPKNTHIFVSWIAQSVTAVAGSGSPFDIVRRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADKGAFFK 271
Db 241 QSGRKGAEIMYSOTIDCWKKIARDEGGAFFR 272

RESULT 14
O44094
ID O44094 PRELIMINARY; PRT; 288 AA.
AC O44094;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE ADP/ATP translocase (Fragment).
GN SESB.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Coneron J.M., Chen B., Kreitman M.;
RL Genetica 0:0-0(1997).
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR FLYBASE; FBgn0023237; Dsub\esb.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mitocarr_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Repeat; Transmembrane; Transport.
FT NON TER 288
SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E47781B26 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
Best Local Similarity 79.6%; Pred. No. 1.6e-102;
Matches 226; Conservative 23; Mismatches 33; Indels 2; Gaps 2;

QY 5 AWSFLKDFLAGAATAVAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRIKPE 64
Db 7 AMGFKDFAAGGISAASVKTAVAPIERVKLLQVQHASKOISAEKQYKGMVDCFIKPE 66
QY 65 QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQFLGGVDHKKQFWRYFAGNLASGGAAG 124
Db 67 QGFSSFWRGNLANVIRYFPTQALNFAFKDKYKQFLGGVDHKKQFWRYFAGNLASGGAAG 126
QY 125 ATSLCFVYPLDFARTLAAADVAGRAQREPHGLGDCIIFKPSDGLRGLYQGFNVSVOGII 184
Db 127 ATSLCFVYPLDFARTLAAADVAGRAQREPHGLGDCIIFKPSDGLRGLYQGFNVSVOGII 186
QY 185 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSYPPDVTVRMMOSGRK 244
Db 187 IYRAAYFGFYDTAR-MLPDPKNTPIYISWIAIAQAVTTVAGIVSYPPDVTVRMMOSGRK 245
QY 245 GADIMYTGTVDCWRKIADKGAFFKAGSNVLRGMGGAFVLV 288
Db 246 ATEIIYKNTIHCWTIAKQEGT-AFFKGAFSNVLRGTGGAFVLV 288

RESULT 15
O44093
ID O44093 PRELIMINARY; PRT; 288 AA.
AC O44093;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

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DE ADP/ATP translocase (Fragment).
GN SESB.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Coneron J.M., Chen B., Kreitman M.;
RL Genetica 0:0-0(1997).
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR FLYBASE; FBgn0023292; Dpse\esb.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mitocarr_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Repeat; Transmembrane; Transport.
FT NON TER 288
SQ SEQUENCE 288 AA; 31725 MW; 052B0CC05043680 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
Best Local Similarity 79.6%; Pred. No. 1.6e-102;
Matches 226; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

QY 5 AWSFLKDFLAGAATAVAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRIKPE 64
Db 7 AMGFKDFAAGGISAASVKTAVAPIERVKLLQVQHASKOISAEKQYKGMVDCFIKPE 66
QY 65 QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQFLGGVDHKKQFWRYFAGNLASGGAAG 124
Db 67 QGFSSFWRGNLANVIRYFPTQALNFAFKDKYKQFLGGVDHKKQFWRYFAGNLASGGAAG 126
QY 125 ATSLCFVYPLDFARTLAAADVAGRAQREPHGLGDCIIFKPSDGLRGLYQGFNVSVOGII 184
Db 127 ATSLCFVYPLDFARTLAAADVAGRAQREPHGLGDCIIFKPSDGLRGLYQGFNVSVOGII 186
QY 185 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSYPPDVTVRMMOSGRK 244
Db 187 IYRAAYFGFYDTAR-MLPDPKNTPIYISWIAIAQAVTTVAGIVSYPPDVTVRMMOSGRK 245
QY 245 GADIMYTGTVDCWRKIADKGAFFKAGSNVLRGMGGAFVLV 288
Db 246 ATEIIYKNTIHCWTIAKQEGS-AFFKGAFSNVLRGTGGAFVLV 288

Search completed: December 30, 2003, 09:56:54
Job time : 43 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 09:54:41 ; Search time 21 Seconds
(without alignments)
598.396 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 1553

Sequence: 1 MGDHWSFLKDFLAGAVAAA.....LRMGGAFLVLYDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1553	100.0	297	4	US-09-434-354-47
2	1457.5	93.9	298	3	US-08-961-871-10
3	1391.5	89.6	298	4	US-09-434-354-48
4	1385.5	89.2	298	4	US-09-434-354-49
5	304	19.6	469	4	US-09-996-243-289
6	301	19.4	469	3	US-09-188-930-339
7	301	19.4	469	4	US-09-312-283C-339
8	291	18.7	447	4	US-09-160-119-4
9	291	18.7	674	4	US-09-160-119-2
10	267	17.2	291	4	US-09-501-558-2
11	265.5	17.1	335	4	US-09-482-273-118
12	238	15.3	320	2	US-08-933-750C-12
13	238	15.0	312	3	US-09-234-613-12
14	233.5	15.0	312	3	US-09-142-565-2
15	227	14.6	299	1	US-08-518-878B-56
16	227	14.6	299	2	US-08-470-868A-56
17	227	14.6	309	1	US-08-518-878B-51
18	227	14.6	309	2	US-08-807-861A-51
19	227	14.6	309	2	US-08-470-868A-51
20	227	14.6	309	3	US-09-210-681-51
21	227	14.6	309	3	US-08-946-719A-51
22	227	14.6	309	4	US-09-547-983-51
23	227	14.6	311	2	US-08-775-009-33
24	225	14.3	311	2	US-08-775-009-32
25	222.5	14.3	308	2	US-08-937-466-2
26	222.5	14.3	308	2	US-09-172-528-2
27	222.5	14.3	308	3	US-09-318-199-2

28	222.5	14.3	308	3	US-09-503-579-2	Sequence 2, Appl
29	218.5	14.1	432	2	US-08-937-466-4	Sequence 4, Appl
30	218.5	14.1	432	2	US-09-172-528-4	Sequence 4, Appl
31	218.5	14.1	432	3	US-09-318-199-4	Sequence 4, Appl
32	218.5	14.1	432	3	US-09-503-579-4	Sequence 4, Appl
33	208.5	13.4	293	4	US-09-501-558-4	Sequence 4, Appl
34	196.5	12.7	307	2	US-08-807-861A-56	Sequence 56, Appl
35	196.5	12.7	307	3	US-09-210-681-56	Sequence 56, Appl
36	196.5	12.7	307	3	US-08-946-719A-56	Sequence 56, Appl
37	196.5	12.7	307	4	US-09-547-983-56	Sequence 56, Appl
38	193	12.4	303	1	US-08-294-522B-36	Sequence 36, Appl
39	192	12.4	303	1	US-08-518-878B-37	Sequence 37, Appl
40	192	12.4	303	2	US-08-807-861A-37	Sequence 37, Appl
41	192	12.4	303	2	US-08-470-868A-37	Sequence 37, Appl
42	192	12.4	303	3	US-09-210-681-37	Sequence 37, Appl
43	192	12.4	303	3	US-08-946-719A-37	Sequence 37, Appl
44	192	12.4	303	4	US-09-547-983-37	Sequence 37, Appl
45	190.5	12.3	306	5	PCT-US94-09799-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-434-354-47

; Sequence 47, Application US/09434354

; Patent No. 6562563

; GENERAL INFORMATION:

; APPLICANT: Murphy, Anne N.

; APPLICANT: Cleverger, William

; APPLICANT: Wiley, Sandra Eileen

; APPLICANT: Andreyev, Alexander Y.

; APPLICANT: Frigeri, Luciano G.

; APPLICANT: Velicelbi, Gonul

; APPLICANT: Davis, Robert E.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING

; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR

; FILE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS

; FILE REFERENCE: 660088.433

; CURRENT APPLICATION NUMBER: US/09/434,354

; CURRENT FILING DATE: 1999-11-03

; NUMBER OF SEQ ID NOS: 54

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 47

; LENGTH: 297

; TYPE: PRT

; ORGANISM: Homo sapien

; US-09-434-354-47

Query Match 100.0%; Score 1553; DB 4; Length 297;

Best Local Similarity 100.0%; Pred. No. 4.2e-172;

Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGDHWSFLKDFLAGAVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVR 60

Db 1 MGDHWSFLKDFLAGAVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVR 60

Qy 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120

Db 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120

Qy 121 GAAGATSLCFVYPLDFAFTRLAADVGRRAQREFHGLGDCIIKIPKSDGLRGLYQGFNVSV 180

Db 121 GAAGATSLCFVYPLDFAFTRLAADVGRRAQREFHGLGDCIIKIPKSDGLRGLYQGFNVSV 180

Qy 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSNWIAQSVTAVAGLLSYPPDTRRRMMQ 240

Db 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSNWIAQSVTAVAGLLSYPPDTRRRMMQ 240

Qy 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRCMGGAFLVLYDEIKKYV 297

Db 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRCMGGAFLVLYDEIKKYV 297

RESULT 2
 US-08-961-871-10
 ; Sequence 10, Application US/08961871
 ; Patent No. 6013858
 ; GENERAL INFORMATION:
 ; APPLICANT: Wallace, Douglas C.
 ; APPLICANT: Graham, Brett H.
 ; APPLICANT: Macgregor, Grant R.
 ; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
 ; Nucleotide Translocator Protein and Methods
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 ; STREET: 5370 Manhattan Circle, Suite 201
 ; CITY: Boulder
 ; STATE: Colorado
 ; COUNTRY: US
 ; ZIP: 80303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/961,871
 ; FILING DATE: 31-OCT-1997
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/030,017
 ; FILING DATE: 01-NOV-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferber, Donna M.
 ; REGISTRATION NUMBER: 33,878
 ; REFERENCE/DOCKET NUMBER: 78-96
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303) 499-8080
 ; TELEFAX: (303) 499-8089
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 298 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-961-871-10

Query Match 93.9%; Score 1457.5; DB 3; Length 298;
 Best Local Similarity 93.6%; Pred. No. 5.4e-161;
 Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
 QY 1 MGDHWSFLKDFLAGAATAVAPIERVVLLQVHASKQISAEKQYKGIIDCVVR 60
 DB 1 MGDHWSFLKDFLAGAATAVAPIERVVLLQVHASKQISAEKQYKGIIDCVVR 60
 QY 61 IPKEQGLSFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRHKQFWRYPAGNLSG 120
 DB 61 IPKEQGLSFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRHKQFWRYPAGNLSG 120
 QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFFHGLGDCIIKI FKS DGLRGLYQGFNVS 179
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFFHGLGDCIIKI FKS DGLRGLYQGFNVS 180
 QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 239
 DB 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 240
 QY 240 QSGRKGADIMYTGTVDCWRKIADEGAKAPFKGANSNVLRCMGGAFFVLVLYDEIKKY 297
 DB 241 QSGRKGADIMYTGTVDCWRKIADEGAKAPFKGANSNVLRCMGGAFFVLVLYDEIKKY 298

RESULT 3
 US-09-434-354-48

; Sequence 48, Application US/09434354
 ; Patent No. 6562563
 ; GENERAL INFORMATION:
 ; APPLICANT: Murphy, Anne N.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Andreyev, Alexander Y.
 ; APPLICANT: Frigeri, Luciano G.
 ; APPLICANT: Velicelebi, Gonul
 ; APPLICANT: Davis, Robert E.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
 ; INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
 ; IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
 ; FILE REFERENCE: 660088.433
 ; CURRENT APPLICATION NUMBER: US/09/434,354
 ; CURRENT FILING DATE: 1999-11-03
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 48
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-434-354-48
 Query Match 89.6%; Score 1391.5; DB 4; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2.5e-153;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MGDHWSFLKDFLAGAATAVAPIERVVLLQVHASKQISAEKQYKGIIDCVVR 60
 DB 1 MGDHWSFLKDFLAGAATAVAPIERVVLLQVHASKQISAEKQYKGIIDCVVR 60
 QY 61 IPKEQGLSFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRHKQFWRYPAGNLSG 120
 DB 61 IPKEQGLSFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRHKQFWRYPAGNLSG 120
 QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFFHGLGDCIIKI FKS DGLRGLYQGFNVS 179
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFFHGLGDCIIKI FKS DGLRGLYQGFNVS 180
 QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 239
 DB 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 240
 QY 240 QSGRKGADIMYTGTVDCWRKIADEGAKAPFKGANSNVLRCMGGAFFVLVLYDEIKKY 296
 DB 241 QSGRKGADIMYTGTVDCWRKIADEGAKAPFKGANSNVLRCMGGAFFVLVLYDEIKKY 297

RESULT 4
 US-09-434-354-49
 ; Sequence 49, Application US/09434354
 ; Patent No. 6562563
 ; GENERAL INFORMATION:
 ; APPLICANT: Murphy, Anne N.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Andreyev, Alexander Y.
 ; APPLICANT: Frigeri, Luciano G.
 ; APPLICANT: Velicelebi, Gonul
 ; APPLICANT: Davis, Robert E.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
 ; INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
 ; IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
 ; FILE REFERENCE: 660088.433
 ; CURRENT APPLICATION NUMBER: US/09/434,354
 ; CURRENT FILING DATE: 1999-11-03
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 49
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Homo sapien

; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
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; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02

; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 19.6%; Score 304; DB 4; Length 469;
Best Local Similarity 29.0%; Pred. No. 1.4e-26;
Matches 88; Conservative 58; Mismatches 115; Indels 42; Gaps 11;
QY 6 WSLKDFLAGAAVAAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVVRIPKEQ 65
Db 187 WRHL---VAGGGAGAVSRTCTAPLDRKVLMOV---HASR-----SNNNGIVGGFTQMIREG 237
QY 66 GFLSFWRGNLAVIRYFPTQALNFAFKDKYKOLFGLGVDR-----HKQFWRYFAGNLASG 120
Db 238 GARSWMRGNGINVLKIAPESATKFMAYEQIKRLV--GSDQETLRIHER-----LVAG 287
QY 121 GAAGATSLCFVYPLDFARTLAAADVGRRAQREFHGLGDCIIKIFKDGDLRLGLYQGFNVSV 180
Db 288 SLAGATAQSSIVPMELKTRMAL-----RKTGYSGMLDCARRILAREGVAAFYKGYVPMN 343
QY 181 QGIIIRAAAYFGVYDTAKGM-----LPDPKNVHFVSWMTAQSVTAVAGLGLSYFFDT 232
Db 344 LGIIPYAGIDLAVYETLKNALQHVAVNSADP---GVFVLLACGTWSTCGQLASYPLAL 400
QY 233 VRRMMMSGRKGADIMYTGTVDCWFKIAKDEGAKAPFKGANSVLRGMGAFV-LVLYD 291
Db 401 VTRMQAASIEGAEPTWSSL--FKHILRTEGAFGLYRGLAPFNKVIPIAVSISYVVE 458
QY 292 EIK 294
Db 459 NLK 461

RESULT 6

US-09-188-930-339
; Sequence 339, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-339

Query Match 19.4%; Score 301; DB 3; Length 469;
Best Local Similarity 28.9%; Pred. No. 3e-26;
Matches 89; Conservative 64; Mismatches 103; Indels 52; Gaps 14;
QY 6 WSLKDFLAGAAVAAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVV-----RI 61
Db 187 WRHL---VAGGGAGAVSRTCTAPLDRKVLMOV---HASRNNM-----CIVGGFTQW 233
QY 62 PKEQGLSFWRGNLAVIRYFPTQALNFAFKDKYKOLFGLGVDR-----HKQFWRYFAGN 116

Db 234 IREGGAKSLWRGNGINVLKIAPESAIFKPMAYEQMKRLV--GSDQETLRIHER-----283
QY 117 LASGGAAGATSLCFVYPLDPTARLTAADVGRRAQREFHGLGDCIIKFKSDGLRGLYQGF 176
Db 284 LVAGSLAGAQAQSIIPMEVLKTRMAL-----RTGQYSGMLDCARRILAKEGVAAPYKGY 339
QY 177 NVSVQGIIRAAAYFGYDPTAKM-----LPDPKNVHIFVSWMIAQSVTAVAG-LLS 227
Db 340 IPNMLGIIPVAGIDLAVYETLKNLQRYAVNSADP---GVFV-LLACGTISSTCCQLAS 395
QY 228 YPFDTVRRMMMSQSGKADIMYTGVDCHRKTADEGAKAFKPGAWSNVLRGMGAFV- 286
Db 396 YPALVTRTRMQAASIEGAPEVTMSSL--FKQILRTEGAFGLYRGLAPNPMKVIPAVSIS 453
QY 287 LVLYDEIK 294
Db 454 YVYENLK 461

RESULT 7

US-09-312-283C-339
; Sequence 339, Application US/09312283C
; Patent No. 6573095

GENERAL INFORMATION:

; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Mouse

US-09-312-283C-339

Query Match 19.4%; Score 301; DB 4; Length 469;
Best Local Similarity 28.9%; Pred. No. 3e-26;
Matches 89; Conservative 64; Mismatches 103; Indels 52; Gaps 14;

QY 6 WSPFKDPLAGAVAAVSKTAVAPIERVKLLQVOHASKQISAEKQYKGIIDCVV----RI 61
Db 187 WRHL---VAGGGAGAVSRTCTAPDLRLKVLNQV-HASRSNNM-----CIVGGFTQM 233
QY 62 PKEQGFLSFRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDR-----HKQFWRYPAGN 116
Db 234 IREGGAKSLWRGNGINVLKIAPESAIFKPMAYEQMKRLV--GSDQETLRIHER-----283
QY 117 LASGGAAGATSLCFVYPLDPTARLTAADVGRRAQREFHGLGDCIIKFKSDGLRGLYQGF 176
Db 284 LVAGSLAGAQAQSIIPMEVLKTRMAL-----RTGQYSGMLDCARRILAKEGVAAPYKGY 339
QY 177 NVSVQGIIRAAAYFGYDPTAKM-----LPDPKNVHIFVSWMIAQSVTAVAG-LLS 227
Db 340 IPNMLGIIPVAGIDLAVYETLKNLQRYAVNSADP---GVFV-LLACGTISSTCCQLAS 395
QY 228 YPFDTVRRMMMSQSGKADIMYTGVDCHRKTADEGAKAFKPGAWSNVLRGMGAFV- 286
Db 396 YPALVTRTRMQAASIEGAPEVTMSSL--FKQILRTEGAFGLYRGLAPNPMKVIPAVSIS 453
QY 287 LVLYDEIK 294
Db 454 YVYENLK 461

RESULT 8

Query Match 18.7%; Score 291; DB 4; Length 674;

US-09-160-119-4
; Sequence 4, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRIL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRT
; ORGANISM: HOMO SAPIENS

Query Match 18.7%; Score 291; DB 4; Length 447;
Best Local Similarity 27.5%; Pred. No. 4.1e-25;
Matches 80; Conservative 53; Mismatches 136; Indels 22; Gaps 7;
QY 12 FLAGAVAAVSKTAVAPIERVKLLQVOHASKQISAEKQYKGIIDCVVRIKPEQGLSPW 71
Db 104 FGLGSVAGAVGATVYPIDLVTRMQNQRSTGSFVGLMYKNSFDCFKKVLRYEGFGLY 163
QY 72 RGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLSGGAAGATSLCFV 131
Db 164 RGLLPOLLGVAPEKAIKLTVDNDFVRDKFM-----HKDGVPLAAETLAGCAGGSQVIFT 218
QY 132 YPLDPTARL--AADV--GRRARQEPHGLGDCIIKFKSDGLRGLYQGFNVSVQGIIR 187
Db 219 NPLEIVKIRLQVAGEITTGFRVS-----ALSVVRDLGFFGIYKGAACACFLRDIPPS 269
QY 188 AAYFGYDPTAKGMLPDPKNVHIFVSWMIAQSVTAV-AGLLSYFPTVRRMMMSQSGRKA 246
Db 270 AIYFPCYAHVKGASFANEDQVSGSLLLAGAAGMPPAASLVTPADVIKTR--LQVAARAG 327
QY 247 DIMYTGTVDCWRKIAKDEGAKAFKPGAWSNVLRGMGG-APVLVLYDEIKKY 296
Db 328 QTTYSGVIDCPKILREEGPKALWKAGARVFRSSPQFGVTLTYELLQRM 378

RESULT 9

US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRIL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: HOMO SAPIENS

US-09-160-119-2

Best Local Similarity	27.5%;	Pred. No.	7.7e-25;
Matches	80;	Conservative	53; Mismatches 136; Indels 22; Gaps 7;
QY	12	FLGAVAAVSKTAVAPIERVKLLLQVHASKQISAEKQYKGIIIDCVVRIRPEQGFLSFW	71
Db	331	FGLGSVAGACATAYVIDLVKTQMQRSTGSPVGELMYKNSPDCKFKVLRYSGFGLY	390
QY	72	RGMLANVIRYFTQALNAPFAKDQKYQLFLGGVDNRHKOFWRFYAGNLASGGAAGATSICFV	131
Db	391	RGLLPQLLGVAPEKAIKLTWNDFVRDKFM-----HKDGSVPLEAIEILLAGGCAGGSQIVTF	445
QY	132	YPLDFARTRL--AADV--GRRAQREFHGLGDCCIIFKSDCLRGLYQGFNVSVQGIILYR	187
Db	446	NPLEIVKIRIQVAGEITTPRVS-----ALUSVVRDLGFFGYKGAKACFTLRDPFS	496
QY	188	AAYFGVYDTAKGMLPDPKNVHI FYSWMIAQSVTAV-AGLLSYPTVRRRMMSGSRKGA	246
Db	497	AIYFP CYAHVKASPANEDGGVSPGCSLLLAGAIAIGMPAASLTVPADVIKTR--LQVAARAG	554
QY	247	DI MYTGVCWRKIADKBEGAKAFPKGAWSNVLRMGG-AFVLVLYDEIKKY	296
Db	555	QTYYSGVIDCFKRILREEGPKALKWKAGARVFRSSPOFGVTLLLYELLOW	605

/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/933,750C
/ FILING DATE: September 23, 1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0356 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 320 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: SPLNOT02
/ CLONE: 207452
/ US-08-933-750C-12

Query Match 15.3%; Score 238; DB 2; Length 320;
Best Local Similarity 23.5%; Pred. No. 3.6e-19;
Matches 71; Conservative 67; Mismatches 124; Indels 40; Gaps 10;
QY 13 LAGAVAAVSKTAVAPIERVKLLQVHAS-KQISAEKQYKGIIDCVRIKPEQGLSEW 71
DB 20 VAGSVGLVTRALISPFVDIKIRFQLOHERLSRSDPSAKYHGLQASRQLQEGPTAW 79
QY 72 RGNLANVIRYFTQALNF-AFKDKYKQLFLGGVDRHKQFWRYPAGNLASGGAAGATSLCF 130
DB 80 KGHVPAQILSIGVAGVQFLSFEMLTENVHRSVYDAREFSVHF-VCGLAACMATLT 135
QY 131 VYPLDFARTLADVRRQAREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIHIIYRAAY 190
DB 136 VHPVDVLRTRFAA---QGEPKVYNTLRHAGVTMYRSEGPQVFKYGLAPTLIAIFPYAGLQ 192
QY 191 FGVDYTAGKMLPDPKKNVHIFVSWMI-----AQSVTAVAGLLSYPPDTVRR 235
DB 193 FSCYSSLK-----HLX-KWAI PAEGKKNENLQNLCCSGAGVISKTLTYPLDLFKK 242
QY 236 RMM-----QSGRK--GADIMYTGTVDCWRKIADKDEGAKAFKFGAWSNVLR-GMGGAFLVL 289
DB 243 RLQVGGFEHARAAGFQVRRYKGLMDCAKQVLOKEGALGFPFKGLSPILLKAAALSTGFMFPS 302
QY 290 YD 291
DB 303 YE 304

RESULT 13
US-09-234-613-12
Sequence 12, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry

/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Corley, Neil C.
/ TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
/ NUMBER OF SEQUENCES: 98
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/234,613
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/933,750
/ FILING DATE: September 23, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0356 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 320 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: SPLNOT02
/ CLONE: 207452
/ US-09-234-613-12

Query Match 15.3%; Score 238; DB 3; Length 320;
Best Local Similarity 23.5%; Pred. No. 3.6e-19;
Matches 71; Conservative 67; Mismatches 124; Indels 40; Gaps 10;
QY 13 LAGAVAAVSKTAVAPIERVKLLQVHAS-KQISAEKQYKGIIDCVRIKPEQGLSEW 71
DB 20 VAGSVGLVTRALISPFVDIKIRFQLOHERLSRSDPSAKYHGLQASRQLQEGPTAW 79
QY 72 RGNLANVIRYFTQALNF-AFKDKYKQLFLGGVDRHKQFWRYPAGNLASGGAAGATSLCF 130
DB 80 KGHVPAQILSIGVAGVQFLSFEMLTENVHRSVYDAREFSVHF-VCGLAACMATLT 135
QY 131 VYPLDFARTLADVRRQAREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIHIIYRAAY 190
DB 136 VHPVDVLRTRFAA---QGEPKVYNTLRHAGVTMYRSEGPQVFKYGLAPTLIAIFPYAGLQ 192
QY 191 FGVDYTAGKMLPDPKKNVHIFVSWMI-----AQSVTAVAGLLSYPPDTVRR 235
DB 193 FSCYSSLK-----HLX-KWAI PAEGKKNENLQNLCCSGAGVISKTLTYPLDLFKK 242
QY 236 RMM-----QSGRK--GADIMYTGTVDCWRKIADKDEGAKAFKFGAWSNVLR-GMGGAFLVL 289
DB 243 RLQVGGFEHARAAGFQVRRYKGLMDCAKQVLOKEGALGFPFKGLSPILLKAAALSTGFMFPS 302
QY 290 YD 291
DB 303 YE 304
RESULT 14
US-09-142-565-2

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; Sequence 2, Application US/09142565A
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Paine
; APPLICANT: Robert James
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142,565A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704551.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 97305305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
; US-09-142-565-2

Query Match      15.0%; Score 233.5; DB 3; Length 312;
Best Local Similarity 24.7%; Pred. No. 1.2e-18;
Matches 73; Conservative 53; Mismatches 145; Indels 25; Gaps 8;

Qy 12 FLAGAVAAVSKTAVAPIERVKLLQVQHASKQISAEK--QYKGIIDCVVRIPKEQGFLS 69
Db 17 FLAGAGTAAACFADLVTFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMTILTMTWRTGPR 76
Qy 70 FWRGNLANVIRYPTQALNFAFKDKYKQLFL-GGVDRHKQFWRYPFAGNLASGGAGATSL 128
Db 77 PYNGLVAGLQRMQSFASIRIGLYDSVKQVTPPKGADNSLTTRILA-----GCTTGAMAV 131
Qy 129 CFVVPDLPFARTLAADV---GRRARQEFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGI 185
Db 132 TCAQPTDVVKVRFOASHLGFPSRDRKYSGTMDAYRTIAREEGVRLWKGTLPNIMRNAI 191
Qy 186 YRAAFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTA-----VAGLLSYPPFTVRRRMMQ 240
Db 192 VNCAEVVYDILKEKLLD---YHLLTDNFPCHFVSAGFCAGCATVVASPVDVVKTRYM-- 246
Qy 241 SGRKGADIMYTGTVDCWRKIADKDEGAKAFPKGANSVLR-GMGGAFVLVLYDEIKK 295
Db 247 ---NSPPGQVFSPLDCMIKMQAEGGTAFYKGTPTSPFLRLGNSWNVVMFVTEQLKR 299

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RESULT 15
US-08-518-878B-56
; Sequence 56, Application US/08518878B
; Patent No. 5702902
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/518,878B
; FILING DATE: 23-AUG-1995

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 299 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-08-518-878B-56

Query Match      14.6%; Score 227; DB 1; Length 299;
Best Local Similarity 23.8%; Pred. No. 6.2e-18;
Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

Qy 12 FLAGAVAAVSKTAVAPIERVKLLQVQHASK---QISAEKQYKGIIDCVVRIPKEQGFL 68
Db 7 FLAGAGTAAACIADLITTFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMTILTMTWRTGPR 66
Qy 69 SFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPFAGNLASGGAGATSL 128
Db 67 SLYNGLVAGLQRMQSFASVIRIGLYDSVKQVTPPKGSEHAS-----IGSRLLAGSTTGALAV 121
Qy 129 CFVVPDLPFARTLAADV---GRRARQEFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGI 188
Db 122 AVAQPTDVVKVRFOASHLGFPSRDRKYSGTMDAYRTIAREEGVRLWKGTSPNARNAI 181
Qy 189 AYFGVYDTAK-----GMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYPPFTVRRRMMQSG 242
Db 182 AELVTVYDLIKDALLKANLMTDDLPCF-FTSAFCAGFCTTV---IASPVDVVKTRYM--- 233
Qy 243 RKGADIMYTGTVDCWRKIADKDEGAKAFPKGANSVLR-GMGGAFVLVLYDEIKK 295
Db 234 -NSALGOYSSAGHCALTMLOKEGPRAFYKGPMPSPFLRLGNSWNVVMFVTEQLKR 286

Search completed: December 30, 2003, 09:58:01
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:57:01 ; Search time 32 Seconds
(without alignments)
1847.131 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 1553

Sequence: 1 MGDHWSFLKDFLAGAVAA.....LRMGAFVLVLYBIKKYV 297

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Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1553	100.0	297	9	US-09-811-094-31
2	1553	100.0	297	9	US-09-810-644-31
3	1553	100.0	297	10	US-09-185-904A-31
4	1391.5	89.6	298	9	US-09-811-094-32
5	1391.5	89.6	298	9	US-09-810-644-32
6	1391.5	89.6	298	10	US-09-185-904A-32
7	1385.5	89.2	298	9	US-09-811-094-33
8	1385.5	89.2	298	9	US-09-810-644-33
9	1385.5	89.2	298	10	US-09-185-904A-33
10	1045.5	67.3	313	12	US-10-369-493-6072
11	1043.5	67.2	313	12	US-10-369-493-6103
12	1037.5	66.8	300	12	US-10-369-493-5919
13	1005.5	64.7	300	12	US-10-369-493-5088
14	773.5	49.8	179	12	US-10-029-386-32501
15	772	49.7	306	12	US-10-369-493-6116

16	771	49.6	301	12	US-10-032-585-7194	Sequence 7194, Ap
17	752.5	48.5	322	12	US-10-369-493-2374	Sequence 2374, Ap
18	745.5	48.0	326	12	US-10-369-493-6333	Sequence 6333, Ap
19	740	47.6	381	12	US-10-141-478A-2	Sequence 2, Appli
20	736	47.4	307	12	US-10-369-493-1450	Sequence 1450, Ap
21	734	47.3	318	10	US-09-801-368-252	Sequence 252, App
22	734	47.3	318	12	US-10-369-493-1421	Sequence 1421, Ap
23	734	47.3	386	9	US-09-734-569-170	Sequence 170, App
24	718.5	46.3	309	12	US-10-369-493-1876	Sequence 1876, Ap
25	706.5	45.5	368	12	US-10-369-493-4217	Sequence 4217, Ap
26	703.5	45.3	308	15	US-10-128-714-3338	Sequence 3338, Ap
27	703.5	45.3	308	15	US-10-128-714-8338	Sequence 8338, Ap
28	676	43.5	298	12	US-10-369-493-6885	Sequence 6885, Ap
29	666	42.9	677	12	US-10-259-165-192	Sequence 192, App
30	461	29.7	132	9	US-09-925-301-1459	Sequence 1459, Ap
31	433.5	27.9	197	12	US-10-369-493-13335	Sequence 13335, A
32	402.5	25.9	87	9	US-09-864-761-36440	Sequence 36440, A
33	350.5	22.6	475	10	US-09-777-921A-4	Sequence 4, Appli
34	346.5	22.3	477	10	US-09-777-921A-2	Sequence 2, Appli
35	320.5	20.6	384	12	US-10-094-749-1789	Sequence 1789, Ap
36	313	20.2	326	12	US-10-369-493-32510	Sequence 22510, A
37	312	20.1	410	10	US-09-777-921A-5	Sequence 5, Appli
38	306	19.7	680	12	US-10-291-172-339	Sequence 339, App
39	304	19.6	469	9	US-09-989-722-289	Sequence 289, App
40	304	19.6	469	9	US-09-989-723-289	Sequence 289, App
41	304	19.6	469	9	US-09-989-279-289	Sequence 289, App
42	304	19.6	469	9	US-09-989-727-289	Sequence 289, App
43	304	19.6	469	10	US-09-989-731-289	Sequence 289, App
44	304	19.6	469	10	US-09-989-732-289	Sequence 289, App
45	304	19.6	469	10	US-09-991-073-289	Sequence 289, App

ALIGNMENTS

RESULT 1

US-09-811-094-31
; Sequence 31, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yashong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT)
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 66088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-31

Query Match	100.0%;	Score 1553;	DB 9;	Length 297;
Best Local Similarity	100.0%;	Pred. No. 2.3e-160;		
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Db	1	MGDHWFLKDFLAGAVAAVKTAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR	60	
Qy	61	IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQKPLFGGVDRHKQFWRYPAGNLAG	120	
Db	61	IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQKPLFGGVDRHKQFWRYPAGNLAG	120	

QY 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
 |||||
 Db 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
 |||||
 QY 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
 |||||
 Db 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
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 QY 241 SGRKGADIMYTGTVDCWRKIADGAKAFKPGAWSNVLGRMGAFVLVLYDEIKKYV 297
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 Db 241 SGRKGADIMYTGTVDCWRKIADGAKAFKPGAWSNVLGRMGAFVLVLYDEIKKYV 297
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RESULT 2

US-09-810-644-31
 ; Sequence 31, Application US/09810644
 ; Patent No. US2002001292A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Willey, Sandra Eileen
 ; APPLICANT: Willey, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; APPLICANT: Pei, Yazhong
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; FILE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
 ; FILE REFERENCE: 660088.420D3
 ; CURRENT APPLICATION NUMBER: US/09/810,644
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 31
 ; LENGTH: 297
 ; TYPE: PRP
 ; ORGANISM: Homo sapien
 US-09-810-644-31

Query Match 100.0%; Score 1553; DB 9; Length 297;
 Best Local Similarity 100.0%; Pred. No. 2.3e-160;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MGDHWSFLKDFLAGAATAVAVSKTAVAPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60
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 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGGVDRHKQFWRYPAGNLSG 120
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 Db 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGGVDRHKQFWRYPAGNLSG 120
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 QY 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
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 Db 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
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 QY 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
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 Db 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
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 QY 241 SGRKGADIMYTGTVDCWRKIADGAKAFKPGAWSNVLGRMGAFVLVLYDEIKKYV 297
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RESULT 3

US-09-185-904A-31
 ; Sequence 31, Application US/09185904A
 ; Patent No. US2002017185A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.

; APPLICANT: Clevenger, William
 ; APPLICANT: Willey, Sandra Eileen
 ; APPLICANT: Willey, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
 ; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
 ; FILE REFERENCE: 660088.420
 ; CURRENT APPLICATION NUMBER: US/09/185,904A
 ; CURRENT FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 31
 ; LENGTH: 297
 ; TYPE: PRP
 ; ORGANISM: Homo sapien
 US-09-185-904A-31

Query Match 100.0%; Score 1553; DB 10; Length 297;
 Best Local Similarity 100.0%; Pred. No. 2.3e-160;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 |||||
 Db 1 MGDHWSFLKDFLAGAATAVAVSKTAVAPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60
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 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGGVDRHKQFWRYPAGNLSG 120
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 Db 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGGVDRHKQFWRYPAGNLSG 120
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 QY 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
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 Db 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
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 QY 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
 |||||
 Db 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
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 QY 241 SGRKGADIMYTGTVDCWRKIADGAKAFKPGAWSNVLGRMGAFVLVLYDEIKKYV 297
 |||||
 Db 241 SGRKGADIMYTGTVDCWRKIADGAKAFKPGAWSNVLGRMGAFVLVLYDEIKKYV 297
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RESULT 4

US-09-811-094-32
 ; Sequence 32, Application US/09811094
 ; Patent No. US20010044144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Willey, Sandra Eileen
 ; APPLICANT: Willey, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; APPLICANT: Pei, Yazhong
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; FILE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
 ; FILE REFERENCE: 660088.420D4
 ; CURRENT APPLICATION NUMBER: US/09/811,094
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 298
 ; TYPE: PRP
 ; ORGANISM: Homo sapien
 US-09-811-094-32

Query Match 89.6%; Score 1391.5; DB 9; Length 298;
 Best Local Similarity 88.6%; Pred. No. 8.6e-143;

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDLFLAGVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
DB 1 MTDAAISPAKDFLAGVAAVSKTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120
QY 121 GAAGATSLCFVYPLDFARTLAAVGR-AOREFHGLGDCIIKIPKSDGLRGLYQGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAAVGR-AOREFHGLGDCIIKIPKSDGLRGLYQGFNVS 180
QY 180 VQGIITYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLTSYPPFTVRRMM 239
DB 181 VQGIITYRAAYFGVYDTAKGMLPDPKNTHIVISWMIATVAVAGLTSYPPFTVRRMM 240
QY 240 QSGRGADIMYTGTVDCWRKIADEGAKAPFKGAWSNVLRGMGGAFVLYLDEIKKY 296
DB 241 QSGRGADIMYTGTVDCWRKIADEGAKAPFKGAWSNVLRGMGGAFVLYLDEIKKY 297

RESULT 5
US-09-810-644-32
; Sequence 32, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yashong
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.4203
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-32

Query Match 89.6%; Score 1391.5; DB 9; Length 298;
Best Local Similarity 88.6%; Pred. No. 8.6e-143;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDLFLAGVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
DB 1 MTDAAISPAKDFLAGVAAVSKTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120
QY 121 GAAGATSLCFVYPLDFARTLAAVGR-AOREFHGLGDCIIKIPKSDGLRGLYQGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAAVGR-AOREFHGLGDCIIKIPKSDGLRGLYQGFNVS 180
QY 180 VQGIITYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLTSYPPFTVRRMM 239
DB 181 VQGIITYRAAYFGVYDTAKGMLPDPKNTHIVISWMIATVAVAGLTSYPPFTVRRMM 240
QY 240 QSGRGADIMYTGTVDCWRKIADEGAKAPFKGAWSNVLRGMGGAFVLYLDEIKKY 296
DB 241 QSGRGADIMYTGTVDCWRKIADEGAKAPFKGAWSNVLRGMGGAFVLYLDEIKKY 297

RESULT 6

US-09-185-904A-32
; Sequence 32, Application US/09185904A
; Patent No. US20020177185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-32

Query Match 89.6%; Score 1391.5; DB 10; Length 298;
Best Local Similarity 88.6%; Pred. No. 8.6e-143;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDLFLAGVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
DB 1 MTDAAISPAKDFLAGVAAVSKTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120
QY 121 GAAGATSLCFVYPLDFARTLAAVGR-AOREFHGLGDCIIKIPKSDGLRGLYQGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAAVGR-AOREFHGLGDCIIKIPKSDGLRGLYQGFNVS 180
QY 180 VQGIITYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLTSYPPFTVRRMM 239
DB 181 VQGIITYRAAYFGVYDTAKGMLPDPKNTHIVISWMIATVAVAGLTSYPPFTVRRMM 240
QY 240 QSGRGADIMYTGTVDCWRKIADEGAKAPFKGAWSNVLRGMGGAFVLYLDEIKKY 296
DB 241 QSGRGADIMYTGTVDCWRKIADEGAKAPFKGAWSNVLRGMGGAFVLYLDEIKKY 297

RESULT 7

US-09-811-094-33
; Sequence 33, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yashong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.4204
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-33

Query Match      89.2%; Score 1385.5; DB 9; Length 298;
Best Local Similarity 87.2%; Pred. No. 3.9e-142;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MGDHWSFLKDFLAGAATAAASVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
Db 1 MTEQAISFAKDFLAGGIAAASKTAVAPIERVKLLQVHASKQIAADKQYKGIIDCVVR 60
Qy 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASG 120
Db 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASG 120
Qy 121 GAAGATSLCFVYPLDFARTLAADVGR- AOREFHGLGDCIIKIFKSDGLRGLYQGFSVS 179
Db 121 GAAGATSLCFVYPLDFARTLAADVGRSGTEREPRGLGDCLVKITKSDGIRGLYQGFSVS 180
Qy 180 VQGIIRYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYFPDVTVRERMM 239
Db 181 VQGIIRYRAAYFGVYDTAKGMLPDPKKNTHIVSWMIAQTAVTAVAGVVSYPDVTVRERMM 240
Qy 240 QSGRKGADIMYTGTVDCWRKIADKGAFFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
Db 241 QSGRKGADIMYTGTVDCWRKIADKGAFFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 8
US-09-810-644-33
; Sequence 33, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yanzhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-33

Query Match      89.2%; Score 1385.5; DB 9; Length 298;
Best Local Similarity 87.2%; Pred. No. 3.9e-142;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MGDHWSFLKDFLAGAATAAASVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
Db 1 MTEQAISFAKDFLAGGIAAASKTAVAPIERVKLLQVHASKQIAADKQYKGIIDCVVR 60
Qy 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASG 120
Db 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASG 120
Qy 121 GAAGATSLCFVYPLDFARTLAADVGR- AOREFHGLGDCIIKIFKSDGLRGLYQGFSVS 179
Db 121 GAAGATSLCFVYPLDFARTLAADVGRSGTEREPRGLGDCIIKIFKSDGLRGLYQGFSVS 180

RESULT 9
US-09-185-904A-33
; Sequence 33, Application US/09185904A
; Patent No. US20020177185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-33

Query Match      89.2%; Score 1385.5; DB 10; Length 298;
Best Local Similarity 87.2%; Pred. No. 3.9e-142;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MGDHWSFLKDFLAGAATAAASVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
Db 1 MTEQAISFAKDFLAGGIAAASKTAVAPIERVKLLQVHASKQIAADKQYKGIIDCVVR 60
Qy 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASG 120
Db 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASG 120
Qy 121 GAAGATSLCFVYPLDFARTLAADVGR- AOREFHGLGDCIIKIFKSDGLRGLYQGFSVS 179
Db 121 GAAGATSLCFVYPLDFARTLAADVGRSGTEREPRGLGDCIIKIFKSDGLRGLYQGFSVS 180
Qy 180 VQGIIRYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYFPDVTVRERMM 239
Db 181 VQGIIRYRAAYFGVYDTAKGMLPDPKKNTHIVSWMIAQTAVTAVAGVVSYPDVTVRERMM 240
Qy 240 QSGRKGADIMYTGTVDCWRKIADKGAFFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
Db 241 QSGRKGADIMYTGTVDCWRKIADKGAFFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 10
US-10-369-493-6072
; Sequence 6072, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
```

;/ TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
;/ FILE REFERENCE: 38-10(52052)B
;/ CURRENT APPLICATION NUMBER: US/10/369,493
;/ CURRENT FILING DATE: 2003-02-28
;/ PRIOR APPLICATION NUMBER: US 60/360,039
;/ PRIOR FILING DATE: 2002-02-21
;/ NUMBER OF SEQ ID NOS: 47374
;/ SEQ ID NO 6072
;/ LENGTH: 313
;/ TYPE: PRT
;/ ORGANISM: Caenorhabditis elegans
;/ US-10-369-493-6072

Query Match 67.3%; Score 1045.5; DB 12; Length 313;
Best Local Similarity 69.4%; Pred. No. 3.9e-105;
Matches 203; Conservative 36; Mismatches 49; Indels 3; Gaps 2;

QY 8 FLKDFLAGAATAVAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGF 67
DB 25 FLIDLASGGTAAAVSKTAVAPIERVKLLQVQDASLTIAADKRYKGIIDVLRVPKEQGY 84

QY 68 LSWRGNLANVIRYFPTQALNFAFKDYKOLFGLGGVDVDRHKQFWRYPAGNLAGSGAAGATS 127
DB 85 AALWRGNLANVIRYFPTQALNFAFKDYKOLFGLGGVDVDRHKQFWRYPAGNLAGSGAAGATS 144

QY 128 LCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIPKSDGLRGLYQGFNVSVQGIYYR 187
DB 145 LCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIPKSDGLRGLYQGFNVSVQGIYYR 204

QY 188 AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYDPFTVRRRMMQSGRKA 246
DB 205 AAYFGMFDATAKMFVTTADGKLNFAAWIAQVVTGSGILSYDPWDTVRRRMMQSGRK-- 262

QY 247 DIMYTGTVDCWRKIADKAGAKAFKGAWSNVLGRMGGAFLVLYDEIKKYV 297
DB 263 DVLKNTLDCAVKLIKNEGMSAMFKGALSNVFRGTGGLVLAIDEIQKFI 313

RESULT 11
US-10-369-493-6103
;/ Sequence 6103, Application US/10369493
;/ Publication No. US20030233675A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Cao, Yongwei
;/ APPLICANT: Hinkle, Gregory J.
;/ APPLICANT: Slater, Steven C.
;/ APPLICANT: Goldman, Barry S.
;/ APPLICANT: Chen, Xianfeng
;/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;/ FILE REFERENCE: 38-10(52052)B
;/ CURRENT APPLICATION NUMBER: US/10/369,493
;/ PRIOR FILING DATE: 2003-02-28
;/ PRIOR APPLICATION NUMBER: US 60/360,039
;/ PRIOR FILING DATE: 2002-02-21
;/ NUMBER OF SEQ ID NOS: 47374
;/ SEQ ID NO 6103
;/ LENGTH: 313
;/ TYPE: PRT
;/ ORGANISM: Caenorhabditis elegans
;/ US-10-369-493-6103

Query Match 67.2%; Score 1043.5; DB 12; Length 313;
Best Local Similarity 69.4%; Pred. No. 6.4e-105;
Matches 202; Conservative 37; Mismatches 49; Indels 3; Gaps 2;

QY 8 FLKDFLAGAATAVAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGF 67
DB 25 FLIDLASGGTAAAVSKTAVAPIERVKLLQVQDASLTIAADKRYKGIIDVLRVPKEQGY 84

QY 68 LSWRGNLANVIRYFPTQALNFAFKDYKOLFGLGGVDVDRHKQFWRYPAGNLAGSGAAGATS 127
DB 85 AALWRGNLANVIRYFPTQALNFAFKDYKOLFGLGGVDVDRHKQFWRYPAGNLAGSGAAGATS 144

QY 128 LCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIPKSDGLRGLYQGFNVSVQGIYYR 187
DB 145 LCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIPKSDGLRGLYQGFNVSVQGIYYR 204

QY 188 AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYDPFTVRRRMMQSGRKA 246
DB 205 AAYFGMFDATAKMFVTTADGKLNFAAWIAQVVTGSGILSYDPWDTVRRRMMQSGRK-- 262

QY 247 DIMYTGTVDCWRKIADKAGAKAFKGAWSNVLGRMGGAFLVLYDEIKKYV 297
DB 263 DVLKNTLDCAVKLIKNEGMSAMFKGALSNVFRGTGGLVLAIDEIQKFI 313

RESULT 12
US-10-369-493-5919
;/ Sequence 5919, Application US/10369493
;/ Publication No. US20030233675A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Cao, Yongwei
;/ APPLICANT: Hinkle, Gregory J.
;/ APPLICANT: Slater, Steven C.
;/ APPLICANT: Goldman, Barry S.
;/ APPLICANT: Chen, Xianfeng
;/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;/ FILE REFERENCE: 38-10(52052)B
;/ CURRENT APPLICATION NUMBER: US/10/369,493
;/ CURRENT FILING DATE: 2003-02-28
;/ PRIOR APPLICATION NUMBER: US 60/360,039
;/ PRIOR FILING DATE: 2002-02-21
;/ NUMBER OF SEQ ID NOS: 47374
;/ SEQ ID NO 5919
;/ LENGTH: 300
;/ TYPE: PRT
;/ ORGANISM: Caenorhabditis elegans
;/ US-10-369-493-5919

Query Match 66.8%; Score 1037.5; DB 12; Length 300;
Best Local Similarity 69.1%; Pred. No. 2.7e-104;
Matches 201; Conservative 38; Mismatches 49; Indels 3; Gaps 2;

QY 8 FLKDFLAGAATAVAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGF 67
DB 12 FLIDLASGGTAAAVSKTAVAPIERVKLLQVQDASLTIAADKRYKGIIDVLRVPKEQGY 71

QY 68 LSWRGNLANVIRYFPTQALNFAFKDYKOLFGLGGVDVDRHKQFWRYPAGNLAGSGAAGATS 127
DB 72 AALWRGNLANVIRYFPTQALNFAFKDYKOLFGLGGVDVDRHKQFWRYPAGNLAGSGAAGATS 131

QY 128 LCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIPKSDGLRGLYQGFNVSVQGIYYR 187
DB 132 LCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIPKSDGLRGLYQGFNVSVQGIYYR 191

QY 188 AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYDPFTVRRRMMQSGRKA 246
DB 192 AAYFGMFDATAKMFVTTADGKLNFAAWIAQVVTGSGILSYDPWDTVRRRMMQSGRK-- 249

QY 247 DIMYTGTVDCWRKIADKAGAKAFKGAWSNVLGRMGGAFLVLYDEIKKYV 297
DB 250 DVLKNTLDCAVKLIKNEGMSAMFKGALSNVFRGTGGLVLAIDEIQKFI 300

RESULT 13
US-10-369-493-5088
;/ Sequence 5088, Application US/10369493
;/ Publication No. US20030233675A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Cao, Yongwei
;/ APPLICANT: Hinkle, Gregory J.
;/ APPLICANT: Slater, Steven C.
;/ APPLICANT: Goldman, Barry S.
;/ APPLICANT: Chen, Xianfeng

1 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
2 FILE REFERENCE: 38-10(52052)B
3 CURRENT APPLICATION NUMBER: US/10/369,493
4 CURRENT FILING DATE: 2003-02-28
5 PRIOR APPLICATION NUMBER: US 60/360,039
6 PRIOR FILING DATE: 2002-02-21
7 NUMBER OF SEQ ID NOS: 47374
8 SEQ ID NO 5088
9 LENGTH: 300
10 TYPE: PRT
11 ORGANISM: Caenorhabditis elegans
12 US-10-369-493-5088

Query Match 64.7%; Score 1005.5; DB 12; Length 300;
Best Local Similarity 66.0%; Pred. No. 8.2e-101;
Matches 192; Conservative 40; Mismatches 56; Indels 3; Gaps 2;
QY 8 FLKDFLAGAAGAAVSTAVAPIERVKLLQVQHASQKQISAEKQYKGIIDCVVRIPKEQGF 67
DB 12 FLVDLAGSGTAAISKATAPIERVKLLQVSDVSETVADKKYKGMVLAARVPEQGY 71
QY 68 LSWRGNLANVIRYPTQALNFAKQKQIFLGVDVDRHKQFWRYPAGNLAGSAGAGATS 127
DB 72 AAFWRGNLANVIRYPTQALNFAKQKQIFLGVDVDRHKQFWRYPAGNLAGSAGAGATS 131
QY 128 LCFVPLDFARTLAADVGRRAQREHGLGDCIKIIFKSDGLRGLYQGFNVSVQGIILYR 187
DB 132 LCFVPLDFARTLAADVGRRAQREHGLGDCIKIIFKSDGLRGLYQGFNVSVQGIILYR 191
QY 188 AAYFGVYDTAKGML-PDPKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMMQSGRKA 246
DB 192 AAYFGVYDTAKGML-PDPKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMMQSGRKA 249
QY 247 DIMYTGTVDCWRKIADKQKAFKAGNSVLRGMGAFVLVLYDEIKKYV 297
DB 250 DILYKNTLDCVRKIVKNEGITALYKGLSNVFRATGALVLTIDYDEIQHLI 300

RESULT 14
US-10-029-386-32501
; Sequence 32501, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32501
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004000.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
; OTHER INFORMATION: SWISSPROT HIT: P05141, EVALUATE 2.00e-83
US-10-029-386-32501

Query Match 49.8%; Score 773.5; DB 12; Length 179;
Best Local Similarity 88.3%; Pred. No. 6.9e-76;
Matches 144; Conservative 12; Mismatches 6; Indels 1; Gaps 1;
QY 38 VQHASQKQISAEKQYKGIIDCVVRIPKEQGFSLFWRGNLANVIRYPTQALNFAKQKQY 97

DB 1 VQHASQKQISAEKQYKGIIDCVVRIPKEQGFSLFWRGNLANVIRYPTQALNFAKQKQY 60
QY 98 LFLGGVDVDRHKQFWRYPAGNLAGSAGAGATS LCFVPLDFARTLAADVGRRAQREHGL 156
DB 61 IFLGVDVDRHKQFWRYPAGNLAGSAGAGATS LCFVPLDFARTLAADVGRRAQREHGL 120
QY 157 GDCIKIIFKSDGLRGLYQGFNVSVQGIILYRAAYFGVYDTAKG 199
DB 121 GDCIKIIFKSDGLRGLYQGFNVSVQGIILYRAAYFGVYDTAKG 163

RESULT 15
US-10-369-493-6116
; Sequence 6116, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6116
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6116

Query Match 49.7%; Score 772; DB 12; Length 306;
Best Local Similarity 51.0%; Pred. No. 2.1e-75;
Matches 150; Conservative 48; Mismatches 90; Indels 6; Gaps 3;
QY 5 AWSFLKDFLAGAAGAAVSTAVAPIERVKLLQVQHASQKQISAEKQYKGIIDCVVRIPKE 64
DB 18 AQKFAIDLLIGVSASVSTVAPIERVKLLQVQSHKDI PADKRYNGIIDAFVVRPKE 77
QY 65 QGFSLFWRGNLANVIRYPTQALNFAKQKQIFLGVDVDRHKQFWRYPAGNLAGSAGAG 124
DB 78 QGFVSWRGNMTNIRYPTQALNFAKQKQIFLGVDVDRHKQFWRYPAGNLAGSAGAG 137
QY 125 ATSLCFVYPLDFARTLAADVGRRAQREHGLGDCIKIIFKSDGLRGLYQGFNVSVQGIIL 184
DB 138 CSSLCIVYPLDFARTLAADVGRRAQREHGLGDCIKIIFKSDGLRGLYQGFNVSVQGIIL 197
QY 185 IYRAAYFGVYDTAKGML-PDPKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMMQSGR 243
DB 198 IYRSVYFGLYDAIRNTINTDKKKLPEYASFAIAQGVTLSSVLTYPDTRRRMMQSGR 256
QY 244 KGADIMYTGTVDCWRKIADKQKAFKAGNSVLRGMGAFVLVLYDEIKKYV 297
DB 257 LSTSKAFSA-----RKIVHEEGVGRGLYKALANIPRSAGGALVMALEYEIHKHM 306

Search completed: December 30, 2003, 10:02:31
Job time: 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:51:25 ; Search time 42 Seconds
(without alignments)
1122.424 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 1553

Sequence: 1 MGDHWSFLKFLAGAVAAA.....LRMGAGFVLVLYDEIKKTV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1553	100.0	297	21	AA171031 Human adenine nucl
2	1553	100.0	297	22	AAU01198 Human adenine nucl
3	1553	100.0	297	23	AAU10378 Human adenine nucl
4	1457.5	93.9	298	19	AAW61169 Anti protein. Mus
5	1442.5	92.9	293	22	ABU53219 Human metabolism-a
6	1398.5	90.1	298	23	AAU18516 Human insulin rece
7	1391.5	89.6	298	21	AA171032 Human adenine nucl
8	1391.5	89.6	298	22	AAU01199 Human adenine nucl
9	1391.5	89.6	298	23	AAU10379 Human adenine nucl

10	1385.5	89.2	298	21	AA171033 Human adenine nucl
11	1385.5	89.2	298	22	AA171033 Human polypeptide
12	1385.5	89.2	298	22	AAU01200 Human adenine nucl
13	1385.5	89.2	298	23	AAU10380 Human adenine nucl
14	1385.5	89.2	323	22	AAU14127 Human polypeptide
15	1294.5	83.4	325	22	ABG15423 Novel human dieno
16	1268.5	83.4	429	24	ABR41715 Human DITHP organe
17	1241	79.9	299	22	ABR66082 Drosophila melanog
18	1241	79.9	299	22	ABR67300 Drosophila melanog
19	1221.5	78.7	263	22	ABG27056 Novel human dieno
20	1147	73.9	307	22	ABR58380 Drosophila melanog
21	1101.5	70.9	315	22	ABU53218 Human metabolism-a
22	1101.5	70.9	315	23	AAE21175 Human TRICH-19 pro
23	926.5	59.7	228	23	ABP43205 Human ovarian anti
24	867.5	55.9	222	23	ABP74106 Human TRICH SEQ ID
25	820	52.8	298	22	ABG18922 Novel human dieno
26	771	49.6	301	23	ABP73357 Candida albicans e
27	746.5	48.1	379	24	ABP81267 Arabidopsis thalia
28	746	48.0	346	21	AA171031 Arabidopsis thalia
29	746	48.0	346	21	AA171031 Arabidopsis thalia
30	746	48.0	346	21	AA171031 Arabidopsis thalia
31	746	48.0	346	21	AA171031 Arabidopsis thalia
32	746	48.0	363	21	AA171031 Arabidopsis thalia
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34	746	48.0	363	21	AA171031 Arabidopsis thalia
35	746	48.0	363	21	AA171031 Arabidopsis thalia
36	746	48.0	381	21	AA171031 Arabidopsis thalia
37	746	48.0	381	21	AA171031 Arabidopsis thalia
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39	746	48.0	381	21	AA171031 Arabidopsis thalia
40	746	48.0	381	21	AA171031 Arabidopsis thalia
41	746	48.0	1009	21	AA171031 Arabidopsis thalia
42	746	48.0	1027	21	AA171031 Arabidopsis thalia
43	743	47.8	346	21	AA171031 Arabidopsis thalia
44	743	47.8	363	21	AA171031 Arabidopsis thalia
45	743	47.8	381	21	AA171031 Arabidopsis thalia

ALIGNMENTS

RESULT 1
AA171031
ID AA171031 standard; Protein; 297 AA.

XX AA171031;

XX 29-AUG-2000 (first entry)

DE Human adenine nucleotide translocator ANTI.

Human; adenine nucleotide translocator; ANTI; mitochondria; ADP; ATP;
adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
mitochondrial permeability transition; neuroprotective; nontropic;
antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
myoclonic epilepsy red ragged fibre syndrome.

OS Homo sapiens.

XX WO200026370-A2.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-US25983.

XX 03-NOV-1998; 98US-0185904.

XX 08-SEP-1999; 99US-0393441.

PA (MITO-) MITOKOR.
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX WPI; 2000-365619/31.
 DR N-PSDB; AAD00519.
 XX Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX Claim 44; Page 172; 175pp; English.
 XX The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MLAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT1 from human brain.
 XX
 SQ Sequence 297 AA;
 Query Match 100.0%; Score 1553; DB 21; Length 297;
 Best Local Similarity 100.0%; Pred. No. 3.4e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGDHWSFLKDFLAGAATAAASVTAPATPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 Db 1 MGDHWSFLKDFLAGAATAAASVTAPATPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 Qy 61 IPKEQGFSLFWRGNLNANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
 Db 61 IPKEQGFSLFWRGNLNANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
 Qy 121 GAAGATSLCFVYPLDFARTLADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
 Db 121 GAAGATSLCFVYPLDFARTLADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
 Qy 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMMQ 240
 Db 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMMQ 240
 Qy 241 SGRKGADIMYTGTVDCWRKIADDEGAKAFKGAWSNVLGRMGGAFLVLYDEIKKYV 297
 Db 241 SGRKGADIMYTGTVDCWRKIADDEGAKAFKGAWSNVLGRMGGAFLVLYDEIKKYV 297
 RESULT 2
 AAU01198
 ID AAU01198 standard; Protein; 297 AA.
 XX
 AC AAU01198;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-1 (ANT-1) protein.
 XX Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX OS Homo sapiens.
 XX WO200132876-A2.
 XX 10-MAY-2001.
 XX 03-NOV-2000; 2000WO-US30535.
 XX 03-NOV-1999; 99US-0434354.
 XX (MITO-) MITOKOR.
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Velicelebi G, Davis RE;
 DR WPI; 2001-291054/30.
 DR N-PSDB; AAS05901.
 XX New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX Disclosure; Fig 2; 186pp; English.
 XX The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 297 AA;
 Query Match 100.0%; Score 1553; DB 22; Length 297;
 Best Local Similarity 100.0%; Pred. No. 3.4e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGDHWSFLKDFLAGAATAAASVTAPATPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 Db 1 MGDHWSFLKDFLAGAATAAASVTAPATPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 Qy 61 IPKEQGFSLFWRGNLNANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
 Db 61 IPKEQGFSLFWRGNLNANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
 Qy 121 GAAGATSLCFVYPLDFARTLADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
 Db 121 GAAGATSLCFVYPLDFARTLADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
 Qy 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMMQ 240
 Db 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMMQ 240
 Qy 241 SGRKGADIMYTGTVDCWRKIADDEGAKAFKGAWSNVLGRMGGAFLVLYDEIKKYV 297
 Db 241 SGRKGADIMYTGTVDCWRKIADDEGAKAFKGAWSNVLGRMGGAFLVLYDEIKKYV 297

RESULT 3
AAU10378
ID AAU10378 standard; Protein; 297 AA.
AC AAU10378;
XX
XX
XX
DT 14-FEB-2002 (first entry)
XX
XX Human adenine nucleotide translocator 1 (ANT1).
DE
XX
XX Human; adenine nucleotide translocator; ANT;
KW mitochondrial matrix protein.
XX
OS Homo sapiens.
XX
XX W0200185944-A2.
PN
XX
PD 15-NOV-2001.
XX
XX 11-MAY-2001; 2001WO-US15416.
XX
XX 11-MAY-2000; 2000US-0569337.
PR
XX
XX (MITO-) MITOKOR.
PA
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
XX
XX
DR WPI; 2002-055598/07.
DR N-PSDB; AAS16688.
XX
XX Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide
XX
XX Claim 44; Fig 2; 147pp; English.
XX
XX The invention relates to a recombinant expression construct (I)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ATP synthesised in the mitochondrial
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (I) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT1.
XX
SQ Sequence 297 AA;
Query Match 100.0%; Score 1553; DB 23; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.4e-173;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGDHWSFLKDFLAGA VAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
DB 1 MGDHWSFLKDFLAGA VAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
DB 61 IPKEQGLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIHKIPKSGDLRGLYQGFNVSV 180
DB 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIHKIPKSGDLRGLYQGFNVSV 180

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QY 181 QGIIYYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSYFPDVTVRRRMMQ 240
DB 181 QGIIYYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSYFPDVTVRRRMMQ 240
QY 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFPKGANSVLRGMGAFVLVLYDEIKKYV 297
DB 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFPKGANSVLRGMGAFVLVLYDEIKKYV 297

RESULT 4
AAW61169
ID AAW61169 standard; Protein; 298 AA.
XX
XX AAW61169;
DT 28-SEP-1998 (first entry)
XX
XX ANT1 protein.
DE
XX
XX ANT1; Adenine nucleotide translocator; cloning; screening;
KW DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation;
KW probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
KW hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
KW lactic acidosis; degenerative muscle disease.
XX
XX Mus sp.
XX
XX W09819714-A1.
PN
XX
XX 14-MAY-1998.
PD
XX
XX 31-OCT-1997; 97WO-US19882.
PF
XX
XX 01-NOV-1996; 96US-0030017.
PR
XX
XX (UYEM-) UNIV EMORY.
PA
XX
XX Graham BC, Macgregor GR, Wallace DC;
PI
XX
XX WPI; 1998-286608/25.
DR N-PSDB; AAV36479.
XX
XX Mice lacking heart-muscle adenine nucleotide translocator protein -
PT useful as model for mitochondrial myopathy and hypertrophic
PT cardiomyopathy in animals and to test therapeutic compositions or
PT gene therapies
XX
XX Disclosure; Page 39-40; 61pp; English.
XX
XX The present sequence is the mouse ANT1 protein, the cDNA producing this
CC polypeptide is cloned by screening a mouse heart cDNA library with the
CC human ANT1 cDNA as a probe. The ANT1 cDNA sequence was determined by DNA
CC Taq dideoxy terminator cycle sequencing. The ANT1 protein is encoded by the
CC ANT1 locus, a nuclear gene on chromosome 8. This protein is required
CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
CC which can then be converted into ATP. An ANT1 homozygous mutant would
CC thus be defective in OXPHOS which results in disease in oxidative
CC metabolism dependent tissues. This mouse ANT1 homozygous mutant can be
CC used as a model system for fascioscapular humeral muscular dystrophy,
CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
CC systems can be used to test possible therapeutic compounds which
CC increase/mediate ATP and ADP exchange across the mitochondrial membrane
CC independent of ANT1.
XX
SQ Sequence 298 AA;
Query Match 93.9%; Score 1457.5; DB 19; Length 298;
Best Local Similarity 93.6%; Pred. No. 5.4e-162;
Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
QY 1 MGDHWSFLKDFLAGA VAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
DB 1 MGDHWSFLKDFLAGA VAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60

QY 61 IPKEQFLSWRGNLANVIRYFPTQALNFAFKDKYKQFLGGVDRHKQFWRYPAGNLASG 120
 DB 61 IPKEQFLSWRGNLANVIRYFPTQALNFAFKDKYKQFLGGVDRHKQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFTRLAADVGR-RAQRFHGLGDCIHKIFKSDGLRGLYQGPNVSV 179
 DB 121 GAAGATSLCFVYPLDFAFTRLAADVGR-RAQRFHGLGDCIHKIFKSDGLRGLYQGPNVSV 180
 QY 180 VOGIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMTAQSVTAVAGLLSYFPDTRRRMM 239
 DB 181 VOGIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMTAQSVTAVAGLLSYFPDTRRRMM 240
 QY 240 QSGRKADIMYTGTCWRKRIADKGAFFKGAWSNVLRGMCAGFVLYLYDEIKKY 297
 DB 241 QSGRKADIMYTGTCWRKRIADKGAFFKGAWSNVLRGMCAGFVLYLYDEIKKY 298

RESULT 5
 ABUS3219
 ID ABUS3219 standard; Protein; 293 AA.
 XX
 AC ABUS3219;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Human metabolism-associated DKFphtes3_35n12 homologue #1.
 XX
 KW Human; gene therapy; vaccine; disease treatment; detection.
 XX
 OS Homo sapiens.
 XX
 PN WO200112659-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 18-AUG-2000; 2000WO-1B01496.
 XX
 PR 18-AUG-1999; 99US-0149499.
 PR 28-SEP-1999; 99US-0156503.
 XX
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
 XX
 PI Wiemann S;
 XX
 DR WPI; 2001-327840/34.
 XX
 XX Nucleic acids having the sequences of clones isolated from libraries of
 PT different human tissues, useful in recombinant DNA methodologies -
 XX
 PS Example III; Page 850; 1095pp; English.
 XX
 CC This invention describes novel polynucleotides and polypeptides isolated
 CC from human cDNA libraries which can be used for gene therapy or in
 CC vaccines. The polynucleotides of the invention and antibodies encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The products of the
 CC invention may also be used to identify modulators of expression and
 CC activity and to down regulate expression and activity. The antibodies of
 CC the invention may also be used as diagnostic agents for detecting the
 CC presence of polypeptides in samples. This sequence represents a homologue
 CC of a polypeptide described in the disclosure of the invention.
 XX
 SQ Sequence 293 AA;

Query Match 92.9%; Score 1442.5; DB 22; Length 293;
 Best Local Similarity 94.2%; Pred. No. 3e-160;
 Matches 276; Conservative 10; Mismatches 6; Indels 1; Gaps 1;
 QY 5 AWSFLKDFLAGAATAVAVPIERVKLLLOVHASKQISAEKQYKGIIDCVRIKPE 64
 DB 1 ALSFLKDFLAGGATAVAVPIERVKLLLOVHASKQISAEKQYKGIIDCVRIKPE 60

QY 65 QGFLSWRGNLANVIRYFPTQALNFAFKDKYKQFLGGVDRHKQFWRYPAGNLASGAG 124
 DB 61 QGFLSWRGNLANVIRYFPTQALNFAFKDKYKQFLGGVDRHKQFWRYPAGNLASGAG 120
 QY 125 ATSLCFVYPLDFAFTRLAADVGR-RAQRFHGLGDCIHKIFKSDGLRGLYQGPNVSVQGI 183
 DB 121 ATSLCFVYPLDFAFTRLAADVGR-RAQRFHGLGDCIHKIFKSDGLRGLYQGPNVSVQGI 180
 QY 184 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMTAQSVTAVAGLLSYFPDTRRRMMQSGR 243
 DB 181 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMTAQSVTAVAGLLSYFPDTRRRMMQSGR 240
 QY 244 KGADIMYTGTCWRKRIADKGAFFKGAWSNVLRGMCAGFVLYLYDEIKKY 296
 DB 241 KGADIMYTGTCWRKRIADKGAFFKGAWSNVLRGMCAGFVLYLYDEIKKY 293

RESULT 6
 AAO18516
 ID AAO18516 standard; Protein; 298 AA.
 XX
 AC AAO18516;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 DE Human insulin receptor signaling modifier SEQ ID NO: 54.
 XX
 KW Human; insulin receptor signaling; insulin receptor signaling modifier;
 KW ISM; diabetes; metabolic syndrome; antidiabetic.
 XX
 OS Homo sapiens.
 XX
 PN WO200255664-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 11-JAN-2002; 2002WO-US01048.
 XX
 PR 12-JAN-2001; 2001US-261226P.
 PR 12-JAN-2001; 2001US-261303P.
 PR 12-JAN-2001; 2001US-261304P.
 PR 12-JAN-2001; 2001US-261335P.
 PR 12-JAN-2001; 2001US-261336P.
 PR 12-JAN-2001; 2001US-261361P.
 PR 12-JAN-2001; 2001US-261456P.
 PR 12-JAN-2001; 2001US-261457P.
 PR 12-JAN-2001; 2001US-261458P.
 PR 12-JAN-2001; 2001US-261459P.
 PR 12-JAN-2001; 2001US-261461P.
 PR 12-JAN-2001; 2001US-261518P.
 PR 12-JAN-2001; 2001US-261531P.
 PR 12-JAN-2001; 2001US-261532P.
 PR 12-JAN-2001; 2001US-261589P.
 PR 12-JAN-2001; 2001US-261590P.
 PR 12-JAN-2001; 2001US-261694P.
 PR 12-JAN-2001; 2001US-261695P.
 PR 12-JAN-2001; 2001US-261697P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Seidel-Dugan C, Ferguson KC, Kidd T;
 XX
 DR WPI; 2002-599664/64.
 DR N-PSDB; AAL48635.
 XX

PT Identifying an insulin receptor signaling modulator, useful as drug
 PT targets for treating diabetes or metabolic disorders, comprises
 PT contacting an assay system comprising insulin receptor signaling
 PT modifiers with a test agent -
 XX
 PS Disclosure; Page 160-161; 232pp; English.
 XX
 CC The present invention relates to a method of identifying a candidate

CC insulin receptor (INR) signaling modulating agent, involving contacting
CC an assay system comprising an insulin receptor signaling modifier (ISM)
CC polypeptide or nucleic acid with a test agent, and detecting a test
CC agent-biased activity of the assay system. The method is useful for
CC identifying candidate INR signaling modulating agents. ISM genes may be
CC used as drug targets for treatment of disorders related to INR signaling
CC such as diabetes or metabolic syndrome. ISM nucleic acids and
CC polypeptides are useful for identifying and testing agents that modulate
CC INR function and for other applications related to the involvement of ISM
CC in INR signaling, and for identifying subjects having a predisposition to
CC such diseases associated with INR signaling. The present sequence is an
CC ISM protein described in the exemplification of the invention.

XX SQ Sequence 298 AA;
XX Query Match 90.1%; Score 1398.5; DB 23; Length 298;
XX Best Local Similarity 88.9%; Pred. No. 4.5e-155;
XX Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;
QY 1 MGDHAWFLKDFLAGAVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
DB 1 MTDAVVSFAKDFLAGGVAIAISKTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKYKOLFGLGVDRHKKQFWRYPAGNLAG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKYKOLFGLGVDRHKKQFWRYPAGNLAG 120
QY 121 GAAGATSLCFVYPLDFARTLAAADVGR-AOREPHGLGDCIIKIFKSDGLRGLYQGNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAAADVGR-AOREPHGLGDCIIKIFKSDGLRGLYQGNVS 180
QY 180 VQGIIRYAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 239
DB 181 VQGIIRYAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 240
QY 240 QSGRKGADIMYTGTCVDCWRKIADKGAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 296
DB 241 QSGRKGTDIMYTGTCVDCWRKIADKGAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 297

RESULT 7
AAV71032
ID AAV71032 standard; Protein; 298 AA.
AC AAV71032;
XX 29-AUG-2000 (first entry)
XX Human adenine nucleotide translocator ANT2.
XX Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
XX adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
XX mitochondrial permeability transition; neuroprotective; nootropic;
XX antiparkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic;
XX antiproliferative; cerebroprotective; therapeutic; screening; psoriasis;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
XX diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
XX mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
XX mitochondrial diabetes and deafness; hyperproliferative disorder;
XX myoclonic epilepsy red ragged fibre syndrome.

XX Homo sapiens.
XX WO200026370-A2.
XX 11-MAY-2000.
XX 03-NOV-1999; 99WO-US25883.
XX 03-NOV-1998; 98US-0185904.
XX 08-SEP-1999; 99US-0393441.
XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Willey SE, Miller SW, Szabo TR;
PI Ghosh SS;
XX WPI; 2000-365619/31.
DR N-PSDB; AAD00520.
XX Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX Claim 45; Page 172-173; 175pp; English.
XX The patent discloses a method to produce adenine nucleotide translocator
CC proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT2 from human brain.

XX SQ Sequence 298 AA;
XX Query Match 89.6%; Score 1391.5; DB 21; Length 298;
XX Best Local Similarity 88.8%; Pred. No. 3e-154;
XX Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
QY 1 MGDHAWFLKDFLAGAVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
DB 1 MTDAVVSFAKDFLAGGVAIAISKTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKYKOLFGLGVDRHKKQFWRYPAGNLAG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKYKOLFGLGVDRHKKQFWRYPAGNLAG 120
QY 121 GAAGATSLCFVYPLDFARTLAAADVGR-AOREPHGLGDCIIKIFKSDGLRGLYQGNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAAADVGR-AOREPHGLGDCIIKIFKSDGLRGLYQGNVS 180
QY 180 VQGIIRYAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 239
DB 181 VQGIIRYAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 240
QY 240 QSGRKGADIMYTGTCVDCWRKIADKGAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 296
DB 241 QSGRKGTDIMYTGTCVDCWRKIADKGAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 297

RESULT 8
AAU01199
ID AAU01199 standard; Protein; 298 AA.
XX AAU01199;
XX 07-SEP-2001 (first entry)
XX Human adenine nucleotide translocator-2 (ANT-2) protein.
XX Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
XX mitochondrial permeability transition pore component; cell survival;
XX mitochondrial core component; mitochondrial related disorder; cancer;
XX Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

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OS Homo sapiens.
XX WO200132876-A2.
XX 10-MAY-2001.
XX 03-NOV-2000; 2000WO-US30535.
XX 03-NOV-1999; 99US-0434354.
XX (MITO-) MITOKOR.
XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
XX Velicelebi G, Davis RE;
XX WPI; 2001-291054/30.
XX N-PSDB; AAS05902.
XX
XX New nucleic acid expression constructs, useful for screening for agents
XX PT that alter mitochondrial permeability transition (MPT), comprises
XX PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
XX PT fused to energy transfer molecule -
XX
XX Disclosure; Fig 2; 186pp; English.
XX
XX The present sequence represents human adenine nucleotide translocator-2
XX (ANT-2) protein. ANT proteins are mitochondrial permeability
XX transition (MTP) pore components responsible for mediating transport
XX of ADP across the mitochondrial inner membrane. ANT proteins interact
XX with other mitochondrial core components e.g. cyclophilins to
XX regulate MPT. The present invention relates to a novel nucleic acid
XX expression construct comprising a promoter operably linked to a
XX polynucleotide encoding a mitochondrial pore component polypeptide
XX (e.g. ANT) fused to an energy transfer molecule (ETM) protein
XX (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
XX expression construct can alter mitochondrial membrane permeability
XX transition and/or alter the interaction between mitochondrial core
XX components. The methods are useful for screening for agents that alter
XX MPT and/or cell survival. These agents are useful for the prevention or
XX treatment of diseases associated with altered mitochondrial function or
XX dysfunctional cell survival, such as Alzheimer's disease, diabetes
XX mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
XX mitochondrial encephalopathy, lactic acidosis, stroke,
XX hyperproliferative disorders e.g. cancer, and deafness.
XX
XX Sequence 298 AA;
XX
Query Match 89.6%; Score 1391.5; DB 22; Length 298;
Best Local Similarity 88.6%; Pred. No. 3e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
QY 1 MGDHANSFLKDFLAGAFAAASVKTAVAPIERVKLLQVQHASQKQISAEKQYKGIIDCVVR 60
DB 1 MTDAAISFAKDFLAGGVAIAISKTAVAPIERVKLLQVQHASQKQITADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGQVDRHKQFWRYPAGNLASG 120
DB 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGQVDRHKQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNV 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNV 180
QY 180 VQGIIRYRAAYFGYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 239
DB 181 VQGIIRYRAAYFGYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 240
QY 240 QSGRKADIMYTGTVDCWRKIADDEGAKAFKGAWSNVLRGMGSAFVLVLYDEIKKY 296
DB 241 QSGRKADIMYTGTVDCWRKIADDEGAKAFKGAWSNVLRGMGSAFVLVLYDEIKKY 297
XX
RESULT 9

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AAU10379
ID AAU10379 standard; Protein; 298 AA.
XX
XX AAU10379;
XX
XX 14-FEB-2002 (first entry)
XX
XX Human adenine nucleotide translocator 2 (ANT2).
XX
XX Human; adenine nucleotide translocator; ANT; ss;
XX KW mitochondrial matrix protein.
XX
XX Homo sapiens.
XX
XX WO200185944-A2.
XX
XX 15-NOV-2001.
XX
XX 11-MAY-2001; 2001WO-US15416.
XX
XX 11-MAY-2000; 2000US-0569327.
XX
XX (MITO-) MITOKOR.
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
XX Ghosh SS, Moos WH, Pei Y, Carroll AK;
XX WPI; 2002-055598/07.
XX N-PSDB; AAS16689.
XX
XX Novel recombinant expression construct for producing adenine nucleotide
XX translocator polypeptides, comprises a regulated promoter linked to
XX nucleic acid encoding the polypeptide -
XX
XX Claim 44; Fig 2; 147pp; English.
XX
XX The invention relates to a recombinant expression construct (I)
XX comprising a regulated promoter operably linked to a nucleic acid
XX encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
XX proteins mediate the exchange of ADP synthesised in the mitochondrial
XX matrix for ADP in the cytosol. (I) is useful for producing recombinant
XX ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
XX culturing the host cell. (I) is also useful for targeting a polypeptide
XX of interest to a mitochondrial membrane, where ANT polypeptide is
XX expressed as a fusion protein with the polypeptide of interest.
XX Recombinant ANT polypeptide, or cells expressing the polypeptide, is
XX useful for identifying an agent that binds to an ANT polypeptide. ANT
XX ligand is useful for determining the presence of an ANT polypeptide,
XX preferably ANTI, ANT2 or ANT3 in a biological sample and for isolating
XX ANT from a biological sample, where the ANT ligand is covalently or non-
XX covalently bound to a solid phase. Detectably labeled ANT ligand is also
XX useful for identifying an agent that interacts with an ANT polypeptide.
XX The present sequence represents the amino acid sequence of human ANT2.
XX
XX Sequence 298 AA;
XX
Query Match 89.6%; Score 1391.5; DB 23; Length 298;
Best Local Similarity 88.6%; Pred. No. 3e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
QY 1 MGDHANSFLKDFLAGAFAAASVKTAVAPIERVKLLQVQHASQKQISAEKQYKGIIDCVVR 60
DB 1 MTDAAISFAKDFLAGGVAIAISKTAVAPIERVKLLQVQHASQKQITADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGQVDRHKQFWRYPAGNLASG 120
DB 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGQVDRHKQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNV 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNV 180
QY 180 VQGIIRYRAAYFGYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 239

```

Db 181 VQGIIRYRAFGIYDTAKMLPDPKNTHTIVISWMIATQVAVAGTSPFDTVRRMM 240
QY 240 QSGRGADIMYTGTVDCWKIKAKDECAKFAFFKGANSVLRGMGAFVLVLYDEIKKY 296
Db 241 QSGRGKTDIMYTGTVDCWKIKARDEGKFAFFKGANSVLRGMGAFVLVLYDEIKKY 297
RESULT 10
AAV71033
ID AAY71033 standard; Protein; 298 AA.
XX AAY71033;
XX
XX 29-AUG-2000 (first entry)
DE Human adenine nucleotide translocator ANT3.
XX Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; norepinephrine;
KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW antipsychotic; cerebroprotective; therapeutic; screening; psoriasis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dysconia;
KW diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW mitochondrial diabetes and deafness; hyperproliferative disorder;
KW myoclonic epilepsy red ragged fibre syndrome.
XX Homo sapiens.
OS
XX
XX WO200026370-A2.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-US25883.
XX
XX 03-NOV-1998; 98US-0185904.
PR 08-SEP-1999; 99US-0393441.
XX
XX (MITO-) MITOKOR.
XX
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;
PI
DR WPI: 2000-365619/31.
DR N-PSDB; AAD00521.
XX
XX Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX
XX Claim 46; Page 173-174; 175pp; English.
XX
XX The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT3 from human brain.
XX
XX Sequence 298 AA;

Query Match c89.2%; Score 1385.5; DB 21; Length 298;
Best Local Similarity .87.2%; Pred. No. 1.5e-153;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
QY 1 MGDHAWSEKDFLAGAVAAAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
Db 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLQVQHASKQIAADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYFPTQALNPAKDKYKQLPGLGGVDRHKOPWRYFAGNLASG 120
Db 61 IPKEQGLSFWRGNLANVIRYFPTQALNPAKDKYKQLPGLGGVDRHKOPWRYFAGNLASG 120
QY 121 GAAGATSLCFVYVPLDFARTRLAADVGR- AQRPHGLGDCIIKIPKSDGLRGLYQGFNVS 179
Db 121 GAAGATSLCFVYVPLDFARTRLAADVGR- AQRPHGLGDCIIKIPKSDGLRGLYQGFNVS 180
QY 180 VQGIIRYRAAFGVYDTAKMLPDPKNTHTIVISWMIATQVAVAGTSPFDTVRRMM 239
Db 181 VQGIIRYRAAFGVYDTAKMLPDPKNTHTIVISWMIATQVAVAGTSPFDTVRRMM 240
QY 240 QSGRGADIMYTGTVDCWKIKAKDEGKFAFFKGANSVLRGMGAFVLVLYDEIKKYV 297
Db 241 QSGRGADIMYTGTVDCWKIKAKDEGKFAFFKGANSVLRGMGAFVLVLYDEIKKYV 298
RESULT 11
AAM39641
ID AAM39641 standard; Protein; 298 AA.
XX AAM39641;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 2786.
XX
XX Human; norepinephrine; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR N-PSDB; AAI58797.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX Example 4; SEQ ID NO 2786; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAI38642-AAI42213) with neurotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 298 AA;
 Query Match 89.2%; Score 1385.5; DB 22; Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.5e-153;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MGDHAWFLKDFLAGAANAASKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 DB 1 MTEQAISFAKDFLAGGIAAISKTAVERVKLLQVHASKQIAADKQYKGIIDCVVR 60
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180
 QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPFTVRRMM 239
 DB 181 VQGIILYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVAAGVVSYPFTVRRMM 240
 QY 240 QSGRGKADIMYTGTVDCWRKIADKGAFFKGAWSNVLRGMGGAFVLYLDEIKKYV 297
 DB 241 QSGRGKADIMYTGTVDCWRKIFRDEGGKAPFKGAWSNVLRGMGGAFVLYLDELKKVI 298
 RESULT 12
 AAU01200
 ID AAU01200 standard; Protein; 298 AA.
 XX
 AC AAU01200;
 DT 07-SEP-2001 (first entry)
 XX Human adenine nucleotide translocator-3 (ANT-3) protein.
 XX Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;

PI Velicelebi G, Davis RE;
 XX
 DR WPI; 2001-291054/30.
 DR N-PSDB; AAS05903.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 298 AA;
 Query Match 89.2%; Score 1385.5; DB 22; Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.5e-153;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MGDHAWFLKDFLAGAANAASKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 DB 1 MTEQAISFAKDFLAGGIAAISKTAVERVKLLQVHASKQIAADKQYKGIIDCVVR 60
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180
 QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPFTVRRMM 239
 DB 181 VQGIILYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVAAGVVSYPFTVRRMM 240
 QY 240 QSGRGKADIMYTGTVDCWRKIADKGAFFKGAWSNVLRGMGGAFVLYLDEIKKYV 297
 DB 241 QSGRGKADIMYTGTVDCWRKIFRDEGGKAPFKGAWSNVLRGMGGAFVLYLDELKKVI 298
 RESULT 13
 AAU10380
 ID AAU10380 standard; Protein; 298 AA.
 XX
 AC AAU10380;
 DT 14-FEB-2002 (first entry)
 XX
 DE Human adenine nucleotide translocator 3 (ANT3).
 XX
 KW Human; adenine nucleotide translocator; ANT;
 KW mitochondrial matrix protein.
 XX
 OS Homo sapiens.


```
XX WO200185944-A2.
XX 15-NOV-2001.
XX 11-MAY-2001; 2001WO-US15416.
XX 11-MAY-2000; 2000US-0569327.
XX (MITO-) MITOKOR.
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
XX Ghosh SS, Moos WH, Pei Y, Carroll AK;
XX WPI; 2002-055598/07.
XX N-PSDB; AAS16690.
XX Novel recombinant expression construct for producing adenine nucleotide
XX translocator polypeptides, comprises a regulated promoter linked to
XX nucleic acid encoding the polypeptide
XX Example 3; Fig 2; 147pp; English.
XX The invention relates to a recombinant expression construct (I)
XX comprising a regulated promoter operably linked to a nucleic acid
XX encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
XX proteins mediate the exchange of ATP synthesised in the mitochondrial
XX matrix for ADP in the cytosol. (I) is useful for producing recombinant
XX ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
XX culturing the host cell. (I) is also useful for targeting a polypeptide
XX of interest to a mitochondrial membrane, where ANT polypeptide is
XX expressed as a fusion protein with the polypeptide of interest.
XX Recombinant ANT polypeptide, or cells expressing the polypeptide, is
XX useful for identifying an agent that binds to an ANT polypeptide. ANT
XX ligand is useful for determining the presence of an ANT polypeptide,
XX preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
XX ANT from a biological sample, where the ANT ligand is covalently or non-
XX covalently bound to a solid phase. Detectably labeled ANT ligand is also
XX useful for identifying an agent that interacts with an ANT polypeptide.
XX The present sequence represents the amino acid sequence of human ANT3.
XX
XX Sequence 298 AA;
XX
XX Query Match 89.2%; Score 1385.5; DB 23; Length 298;
XX Best Local Similarity 87.2%; Pred. No. 1.5e-153;
XX Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
XX
XX QY 1 MGDHAWFLKDFLAGAATAVAVAPIERVKLLQVQHASQKISAEKQYKGIIDCVVR 60
XX Db 1 MTEQAISFAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHASQKIAADKQYKGIIDCVVR 60
XX
XX QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRHKQFWRYPAGNLAG 120
XX Db 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRHKQFWRYPAGNLAG 120
XX
XX QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AQRFPFHGLGDCIIIFKSDGRLGILYQGFNVS 179
XX Db 121 GAAGATSLCFVYPLDFARTLAADVGR-AQRFPFHGLGDCIIIFKSDGRLGILYQGFNVS 180
XX
XX QY 180 VQGIILYRAAYFGYDTAKMLPDPKXNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 239
XX Db 181 VQGIILYRAAYFGYDTAKMLPDPKXNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 240
XX
XX QY 240 QSGRKGADIMYTGTVDCWRKIIFRDEGKAFKGAWSNVLKMGAFVLVLYDLKKVY 297
XX Db 241 QSGRKGADIMYTGTVDCWRKIIFRDEGKAFKGAWSNVLKMGAFVLVLYDLKKVY 298
XX
XX RESULT 14
XX AAM41427
XX ID AAM41427 standard; Protein; 323 AA.
XX
XX AC AAM41427;
XX
XX 22-OCT-2001 (first entry)
XX Human polypeptide SEQ ID NO 6358.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX
XX Homo sapiens.
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-052317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX N-PSDB; AAI60583.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries
XX
XX Example 2; SEQ ID NO 6358; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
XX the encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.
XX
XX Sequence 323 AA;
XX
XX Query Match 89.2%; Score 1385.5; DB 22; Length 323;
XX Best Local Similarity 87.2%; Pred. No. 1.7e-153;
XX Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
XX
XX QY 1 MGDHAWFLKDFLAGAATAVAVAPIERVKLLQVQHASQKISAEKQYKGIIDCVVR 60
XX Db 26 MTEQAISFAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHASQKIAADKQYKGIIDCVVR 85
XX
XX QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRHKQFWRYPAGNLAG 120
XX Db 86 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRHKQFWRYPAGNLAG 145
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121 GAAGATSLCFVYPLDFAFTRLAADVRR-AQREPHGLGDCIIKIFKSDGLRGGLYQGFNVS 179
|||||
146 GAAGATSLCFVYPLDFAFTRLAADVRR-AQREPHGLGDCIIKIFKSDGLRGGLYQGFNVS 205
|||||
180 VQGIIRYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 239
|||||
206 VQGIIRYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 265
|||||
240 QSGRKGADIMYTGTVDCWRKIADGAKAFKGAWSNVLRGMGAFVLVLYDEIKKV 297
|||||
266 QSGRKGADIMYTGTVDCWRKIADGAKAFKGAWSNVLRGMGAFVLVLYDEIKKV 323
|||||

RESULT 15
ABG15423
ID ABG15423 standard; Protein; 325 AA.
XX AC ABG15423;
XX
XX 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #15414.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI
XX
XX WPI; 2001-639362/73.
DR
DR N-PSDB; AAS79610.
XX
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
XX
PS Claim 20; SEQ ID No 45782; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 325 AA;
Query Match 83.4%; Score 1294.5; DB 22; Length 325;
Best Local Similarity 83.4%; Pred. No. 8e-143;
Matches 251; Conservative 19; Mismatches 26; Indels 5; Gaps 4;
Qy 1 MGDHWSFLKDFLAGAVAAVSKTAVAPIERVKLLQVOHASKQISAEKQYKGIIDCVVR 60
Db 24 MTDAAVSFAKDFLAGGVAASISKTAVAPIERVKLLQVOHASKQIAADQYKGIIDCVVR 83
Qy 61 IPKEQGFSLFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
Db 84 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 143
Qy 121 GAAGATSLCFVYPLDFAFTRLAADVRR-AQREPHGLGDCIIKIFKSDGLRGGLYQGFNVS 179
Db 144 GAAGATSLCFVYPLDFAFTRLAADVRR-AQREPHGLGDCIIKIFKSDGLRGGLYQGFNVS 203
Qy 180 VQGIIRYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSV-TAVAGLLSYFPDTRRR 236
Db 204 VQGIIRYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSV-TAVAGLLSYFPDTRRR 263
Qy 237 MMQSGRKGADIMYTGTVDCWRKIADGAKAFKGAWSNVLRGMGAFVLVLYD-EIKK 295
Db 264 EXMQSGRKGADIMYTGTVDCWRKIADGAKAFKGAWSNVLRGMGAFVLVLYD-EIKK 323
Qy 296 Y 296
Db 324 Y 324

Search completed: December 30, 2003, 09:55:59
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:53:51 ; Search time 21 Seconds
(without alignments)

1360.100 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 1553

Sequence: 1 MGDHAWFLKDFLAGAVAAA.....LRMGGAFLVLYDEIKKTV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1526.5	98.3	298	1 A44778	ADP,ATP carrier pr
2	1466.5	94.4	298	2 I60173	adenine nucleotide
3	1463.5	94.2	298	2 S37210	ADP,ATP carrier pr
4	1458.5	93.9	298	1 XWBO	ADP,ATP carrier pr
5	1391.5	89.6	298	1 A29132	ADP,ATP carrier pr
6	1385.5	89.2	298	1 S03894	ADP,ATP carrier pr
7	1380.5	88.9	298	2 B43846	ADP,ATP carrier pr
8	1368.5	88.1	298	2 S31814	ADP,ATP carrier pr
9	1142.5	73.6	301	1 S31935	ADP,ATP carrier pr
10	1045.5	67.3	313	2 T25850	hypothetical prote
11	1043.5	67.2	313	2 T23207	hypothetical prote
12	1037.5	66.8	300	2 T25371	hypothetical prote
13	1005.5	64.7	300	2 T15206	hypothetical prote
14	973.5	62.7	339	2 A41677	ADP,ATP carrier pr
15	904.5	58.2	301	2 S51132	ADP,ATP carrier pr
16	772	49.7	306	2 T20012	hypothetical prote
17	770.5	49.6	308	1 S30259	ADP,ATP carrier pr
18	756.5	48.7	387	2 S14876	ADP,ATP carrier pr
19	752.5	48.5	322	2 T40526	ADP,ATP carrier pr
20	752.5	48.5	386	2 T09709	ADP,ATP carrier pr
21	751.5	48.4	387	2 S16568	ADP,ATP carrier pr
22	746.5	48.1	379	2 T04608	ADP,ATP carrier pr
23	746.5	48.1	382	2 S33630	ADP,ATP carrier pr
24	745.5	48.0	326	2 T25728	hypothetical prote
25	745.5	48.0	386	2 S17917	ADP,ATP carrier pr
26	744.5	47.9	386	2 S21374	ADP,ATP carrier pr
27	740	47.6	379	2 S21313	ADP,ATP carrier pr
28	740	47.6	386	2 S14874	ADP,ATP carrier pr
29	737	47.5	385	1 S29852	ADP,ATP carrier pr

ALIGNMENTS

RESULT 1

A44778

ADP,ATP carrier protein T1 - human

N;Alternate names: mitochondrial ADP,ATP translocase 1

C:Species: Homo sapiens (man)

C>Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: A44778; S03893; A39891; A28116

R:Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.;

J. Biol. Chem. 264, 13998-14004, 1989

A>Title: A human muscle adenine nucleotide translocator gene has four exons, is located

A:Reference number: A44778; MUID:89340499; PMID:2547778

A:Accession: A44778

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-298 <LIA>

A:Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659

R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.

J. Mol. Biol. 206, 261-280, 1989

A>Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr

A:Reference number: S03893; MUID:89236396; PMID:2541251

A:Accession: S03893

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-298 <COZ>

R:Neckelmann, N.; Li, X.; Wade, R.P.; Shuster, R.; Wallace, D.C.

Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987

A>Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader

A:Reference number: A39891; MUID:88041149; PMID:2823266

A:Accession: A39891

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>

A:Cross-references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920

A:Experimental source: clone pHMANT

R:Houldsworth, J.; Attardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A:Reference number: A94197; MUID:88124845; PMID:2829183

A:Accession: A28116

A:Molecule type: mRNA

A:Residues: 1-37 <HOU>

A:Cross-references: GB:J03593; NID:g339724; PIDN:AAA36751.1; PID:g339725

A:Experimental source: liver

C:Genetics:

A:Gene: GDB:ANT1; T1

A:Cross-references: GDB:119680; OMIM:103220

A:Map position: 4q35-q435

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

F;2-298/Product: ADP,ATP carrier protein #status predicted <MAT>

F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 98.3%; Score 1526.5; DB 1; Length 298;
Best Local Similarity 98.3%; Pred. No. 1.5e-130; Indels 1; Gaps 1;
Matches 293; Conservative 2; Mismatches 2;
Qy 1 MGDHWSFLKDFLAGAATAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
Db 1 MGDHWSFLKDFLAGGAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
Qy 61 IPKEQGLFSLFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
Db 61 IPKEQGLFSLFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
Qy 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNV 179
Db 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNV 180
Qy 180 VQGIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 239
Db 181 VQGIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 240
Qy 240 QSGRKGADIMYTGTCVDCWRKIADKDEGAKAFKFGAWSNVLRGMGAFVLVLYDEIKKYV 297
Db 241 QSGRKGADIMYTGTCVDCWRKIADKDEGAKAFKFGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 2
160173
adenine nucleotide translocator - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C;Accession: I60173
R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
Biochim. Biophys. Acta 1152, 192-196, 1993
A;Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat
A;Reference number: I60173; MUID:94002161; PMID:8399300
A;Accession: I60173
A;Status: preliminary; translated from GH/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-298 <RES>
A;Cross-references: EMBL:X61667; NID:9400426; PIDN:CAA43842.1; PID:9400427
C;Genetics:
A;Introns: 37/3; 200/1; 247/1
A;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.4%; Score 1466.5; DB 2; Length 298;
Best Local Similarity 94.3%; Pred. No. 4.1e-125;
Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;
Qy 1 MGDHWSFLKDFLAGAATAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
Db 1 MGDHWSFLKDFLAGGAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
Qy 61 IPKEQGLFSLFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
Db 61 IPKEQGLFSLFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
Qy 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNV 179
Db 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNV 180
Qy 180 VQGIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 239
Db 181 VQGIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 240
Qy 240 QSGRKGADIMYTGTCVDCWRKIADKDEGAKAFKFGAWSNVLRGMGAFVLVLYDEIKKYV 297

Db 241 QSGRKGADIMYTGTCVDCWRKIADKDEGAKAFKFGAWSNVLRGMGAFVLVLYDEIKKYV 298
RESULT 3
S37210
ADP,ATP carrier protein T1 - mouse
N;Alternate names: adenine nucleotide carrier
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C;Accession: S37210
R;Leplace, C.; Costet, P.
submitted to the EMBL Data Library, September 1993
A;Reference number: S37210
A;Accession: S37210
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <LAP>
A;Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628
C;Genetics:
A;Gene: ANCI
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1463.5; DB 2; Length 298;
Best Local Similarity 94.0%; Pred. No. 7.6e-125;
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;
Qy 1 MGDHWSFLKDFLAGAATAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
Db 1 MGDHWSFLKDFLAGGAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
Qy 61 IPKEQGLFSLFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
Db 61 IPKEQGLFSLFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120
Qy 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNV 179
Db 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNV 180
Qy 180 VQGIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 239
Db 181 VQGIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 240
Qy 240 QSGRKGADIMYTGTCVDCWRKIADKDEGAKAFKFGAWSNVLRGMGAFVLVLYDEIKKYV 297
Db 241 QSGRKGADIMYTGTCVDCWRKIADKDEGAKAFKFGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 4
XWBO
ADP,ATP carrier protein T1 - bovine
N;Alternate names: ADP/ATP translocase T1
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
C;Accession: A43646; A24822; A03181; A61343; S69369
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: A43646
A;Molecule type: mRNA
A;Residues: 1-298 <POM>
A;Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415
R;Rasmussen, U.B.; Wohlrab, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
A;Reference number: A24822; MUID:86295775; PMID:3017341
A;Accession: A24822
A;Molecule type: mRNA
A;Residues: 208-298 <RAS>

A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID:g162631
 R;Aquila, H.; Misra, D.; Eulitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
 A;Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria
 A;Reference number: A03181; MUID:82198267; PMID:7076130
 A;Accession: A03181
 A;Molecule type: protein
 A;Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <AQ>
 A;Note: residue 52 may be methyllysine
 R;Babel, W.; Wächter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A;Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondria
 A;Reference number: A61343; MUID:82046808; PMID:6271240
 A;Accession: A61343
 A;Molecule type: protein
 A;Residues: 205-298 <BAB>
 R;Oettmeier, W.; Masson, K.; Kalinna, S.
 Eur. J. Biochem. 221, 730-733, 1995
 A;Title: [(3H)7-azido-4-isobutyryl]acridone labels Cys159 of the bovine mitochondrial ADP/ATP carrier
 A;Reference number: S69369; MUID:95172058; PMID:7867632
 A;Accession: S69369
 A;Molecule type: protein
 A;Residues: 49-63;154-168 <OET>
 C;Comment: This protein is synthesized in the cytosol and transported into the mitochondria
 C;Complex: homodimer
 C;Function:
 A;Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP
 A;Note: located in the inner mitochondrial membrane
 C;Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C;Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitochondria
 F;5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F;110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F;207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>
 F;2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F;52/Modified site: N6-methyllysine (lys) #status predicted

Query Match 93.9%; Score 1458.5; DB 1; Length 298;
 Best Local Similarity 94.3%; Pred. No. 2.2e-124;
 Matches 281; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDFLAGAATAVSTAVPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60
 DB 1 MSDQALSFLKDFLAGGVAATAVSTAVPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60

QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLAG 120
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLAG 120

QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 179
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 180

QY 180 VQGIILYRAAYFGYDTAKGMLPDKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 239
 DB 180 VQGIILYRAAYFGYDTAKGMLPDKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 240

QY 240 QSGRKGADIMYTGTVDCWRKIANDGAKAFKFGANSNVLRGMGAFVLVLYDEIKKY 297
 DB 241 QSGRKGADIMYTGTVDCWRKIANDGAKAFKFGANSNVLRGMGAFVLVLYDEIKKY 298

RESULT 5
 A29132
 ADP/ATP carrier protein T2 - human
 N;Alternate names: mitochondrial ADP/ATP translocase 2
 C;Species: Homo sapiens (man)
 C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C;Accession: A29132; C28116
 R;Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 262, 4355-4359, 1987
 A;Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated
 A;Reference number: A29132; MUID:87166056; PMID:3031073
 A;Accession: A29132

A;Molecule type: mRNA
 A;Residues: 1-298 <BAT>
 A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
 R;Houldsworth, J.; Attardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
 A;Reference number: A94197; MUID:88124845; PMID:2829183
 A;Accession: C28116
 A;Molecule type: mRNA
 A;Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
 A;Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; PID:g339721
 A;Experimental source: clone PHAT3
 C;Genetics:
 A;Gene: GDB:ANT2; T3; 2F1
 A;Cross-references: GDB:125190; OMIM:300150
 A;Map position: Xq13-Qx26
 A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:J03591
 C;Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F;5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F;110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F;207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 89.6%; Score 1391.5; DB 1; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2.5e-118;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDFLAGAATAVSTAVPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60
 DB 1 MTDALSPAFKDFLAGGVAATAVSTAVPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60

QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLAG 120
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLAG 120

QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 179
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 180

QY 180 VQGIILYRAAYFGYDTAKGMLPDKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 239
 DB 180 VQGIILYRAAYFGYDTAKGMLPDKNVHIFVSMIAQSVTAVAGLLSYFPDTRRRMM 240

QY 240 QSGRKGADIMYTGTVDCWRKIANDGAKAFKFGANSNVLRGMGAFVLVLYDEIKKY 296
 DB 241 QSGRKGADIMYTGTVDCWRKIANDGAKAFKFGANSNVLRGMGAFVLVLYDEIKKY 297

RESULT 6
 S03894
 ADP/ATP carrier protein T3 - human
 N;Alternate names: ADP/ATP carrier protein T2 (misidentification); mitochondrial ADP/ATP
 C;Species: Homo sapiens (man)
 C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C;Accession: S03894; B28116
 R;Cozens, A.L.; Runswick, M.J.; Walker, J.E.
 J. Mol. Biol. 205, 261-280, 1989
 A;Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr
 A;Reference number: S03893; MUID:89236396; PMID:2541251
 A;Accession: S03894
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-298 <COZ>
 R;Houldsworth, J.; Attardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
 A;Reference number: A94197; MUID:88124845; PMID:2829183
 A;Accession: B28116
 A;Molecule type: mRNA
 A;Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>
 A;Cross-references: GB:J03592; NID:g339722; PIDN:AAA36750.1; PID:g339723
 A;Experimental source: liver
 C;Genetics:

A;Gene: GDB:ANT3; ANT3Y
A;Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F;2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 89.2%; Score 1385.5; DB 1; Length 298;
Best Local Similarity 87.2%; Pred. No. 8.8e-118;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAFAAASVTAVAPIERVKLLQVHASKQIAEAKQYKGIIDCVVR 60
DB 1 MTEQAISFAKDFLAGGIAAASVTAVAPIERVKLLQVHASKQIAEAKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQIFLGVDVDRHGFWRYPAGNLAG 120
DB 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQIFLGVDVDRHGFWRYPAGNLAG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AOREFHGLGDCIIKIFKSDGLRGLYQGNNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AOREFHGLGDCIIKIFKSDGLRGLYQGNNVS 180
QY 180 VQGIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYPPFTVRRMM 239
DB 180 VQGIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYPPFTVRRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADEKAGAFKFGANSNVLRGMGGAFVLVLYDEIKKY 297
DB 240 QSGRKGADIMYTGTVDCWRKIADEKAGAFKFGANSNVLRGMGGAFVLVLYDEIKKY 298

Query Match 88.1%; Score 1368.5; DB 2; Length 298;
Best Local Similarity 87.2%; Pred. No. 3e-116;
Matches 259; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAFAAASVTAVAPIERVKLLQVHASKQIAEAKQYKGIIDCVVR 60
DB 1 MTEQAISFAKDFLAGGIAAASVTAVAPIERVKLLQVHASKQIAEAKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQIFLGVDVDRHGFWRYPAGNLAG 120
DB 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQIFLGVDVDRHGFWRYPAGNLAG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AOREFHGLGDCIIKIFKSDGLRGLYQGNNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AOREFHGLGDCIIKIFKSDGLRGLYQGNNVS 180
QY 180 VQGIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYPPFTVRRMM 239
DB 180 VQGIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYPPFTVRRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADEKAGAFKFGANSNVLRGMGGAFVLVLYDEIKKY 296
DB 240 QSGRKGADIMYTGTVDCWRKIADEKAGAFKFGANSNVLRGMGGAFVLVLYDEIKKY 297

Query Match 88.9%; Score 1380.5; DB 2; Length 298;
Best Local Similarity 86.9%; Pred. No. 2.5e-117;
Matches 259; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAFAAASVTAVAPIERVKLLQVHASKQIAEAKQYKGIIDCVVR 60
DB 1 MTEQAISFAKDFLAGGIAAASVTAVAPIERVKLLQVHASKQIAEAKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQIFLGVDVDRHGFWRYPAGNLAG 120
DB 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQIFLGVDVDRHGFWRYPAGNLAG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AOREFHGLGDCIIKIFKSDGLRGLYQGNNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AOREFHGLGDCIIKIFKSDGLRGLYQGNNVS 180

QY 180 VQGIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYPPFTVRRMM 239
DB 180 VQGIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYPPFTVRRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADEKAGAFKFGANSNVLRGMGGAFVLVLYDEIKKY 297
DB 240 QSGRKGADIMYTGTVDCWRKIADEKAGAFKFGANSNVLRGMGGAFVLVLYDEIKKY 298

RESULT 8
S31814
ADP,ATP carrier protein T2 - mouse
N;Alternate names: adenine nucleotide translocase
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
C;Accession: S31814
R;Cosmet, P.; Laplace, C.
submitted to the EMBL Data Library, January 1993
A;Reference number: S31814
A;Accession: S31814
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <COS>
A;Cross-references: EMBL:X70847
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 88.1%; Score 1368.5; DB 2; Length 298;
Best Local Similarity 87.2%; Pred. No. 3e-116;
Matches 259; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAFAAASVTAVAPIERVKLLQVHASKQIAEAKQYKGIIDCVVR 60
DB 1 MTEQAISFAKDFLAGGIAAASVTAVAPIERVKLLQVHASKQIAEAKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQIFLGVDVDRHGFWRYPAGNLAG 120
DB 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQIFLGVDVDRHGFWRYPAGNLAG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AOREFHGLGDCIIKIFKSDGLRGLYQGNNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AOREFHGLGDCIIKIFKSDGLRGLYQGNNVS 180
QY 180 VQGIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYPPFTVRRMM 239
DB 180 VQGIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYPPFTVRRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADEKAGAFKFGANSNVLRGMGGAFVLVLYDEIKKY 296
DB 240 QSGRKGADIMYTGTVDCWRKIADEKAGAFKFGANSNVLRGMGGAFVLVLYDEIKKY 297

RESULT 9
S31935
ADP,ATP carrier protein - African malaria mosquito
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S31935; S31936
R;Beard, C.B.; Crews-Owen, A.E.; Collins, P.H.
submitted to the EMBL Data Library, February 1993
A;Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae.
A;Reference number: S31935
A;Accession: S31935
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <BEA>
A;Cross-references: EMBL:Z21815
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; transmembrane protein
F;7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 73.6%; Score 1142.5; DB 1; Length 301;
Best Local Similarity 76.2%; Pred. No. 8.8e-96;
Matches 221; Conservative 26; Mismatches 42; Indels 1; Gaps 1;
QY 6 WSLKDFLAGAATAAASKTAVAPIERVKLLLOVQHASQKISAEKQYKGIIDCVVRIPEQ 65
DB 8 YGFAKDFLAGGISAASKTAVAPIERVKLLLOVQHASQKISAEKQYKGIIDCVVRIPEQ 67
QY 66 GFLSFRGNLANVIRYPTQALNFAKDKYKQIFLGVDVRHKKQFWRYPAGNLASGGAAGA 125
DB 68 GIGAFCCGNLANVIRYPTQALNFAKDKYKQIFLGVDVRHKKQFWRYPAGNLASGGAAGA 127
QY 126 TSCFVYPLDFAARLAAVGRRA-OREPHGLGDCIIKIPKSDGLRGLVQGNVSVQGI 184
DB 128 TSCFVYPLDFAARLAAVGRRA-OREPHGLGDCIIKIPKSDGLRGLVQGNVSVQGI 187
QY 185 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPTDVRRRMMQSGRK 244
DB 188 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPTDVRRRMMQSGRK 247
QY 245 GADIMYTGTVDCWRKIADKQKAFKPGAWSNVLRGMGGAFLVLYDEIK 294
DB 248 KSEVMYKNTLDCVVKICKQSGGAFFKGAENLVRGTGGALVLYVYDEVK 297

RESULT 10

T25850
hypothetical protein T01B11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C;Accession: T25850
R;Geisel, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1996
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-313 <GEI>
A;Cross-references: EMBL:U80931; PIDN: AAB38001.1; GSPDB: GN00022; CESP: T01B11.4
A;Experimental source: strain Bristol N2; clone T01B11
C;Genetics:
A;Gene: CESP: T01B11.4
A;Map position: 4
A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1045.5; DB 2; Length 313;
Best Local Similarity 69.8%; Pred. No. 5.6e-87;
Matches 203; Conservative 36; Mismatches 49; Indels 3; Gaps 2;
QY 8 FLKDFLAGAATAAASKTAVAPIERVKLLLOVQHASQKISAEKQYKGIIDCVVRIPEQ 67
DB 25 FLIDLASGGTAASVKTAVAPIERVKLLLOVQHASQKISAEKQYKGIIDCVVRIPEQ 84
QY 68 LSWFRGNLANVIRYPTQALNFAKDKYKQIFLGVDVRHKKQFWRYPAGNLASGGAAGA 127
DB 85 AALWRGNLANVIRYPTQALNFAKDKYKQIFLGVDVRHKKQFWRYPAGNLASGGAAGA 144
QY 128 LCFVYPLDFAARLAAVGRRA-OREPHGLGDCIIKIPKSDGLRGLVQGNVSVQGI 187
DB 145 LCFVYPLDFAARLAAVGRRA-OREPHGLGDCIIKIPKSDGLRGLVQGNVSVQGI 204
QY 188 AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPTDVRRRMMQSGRK 246
DB 205 AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPTDVRRRMMQSGRK 262
QY 247 DIMYTGTVDCWRKIADKQKAFKPGAWSNVLRGMGGAFLVLYDEIK 297
DB 263 DVLYKNTLDCVVKICKQSGGAFFKGAENLVRGTGGALVLYVYDEVK 313

RESULT 11

T23207
hypothetical protein K01H12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C;Accession: T23207
R;McMurray, A.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19707
A;Accession: T23207
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-313 <WIL>
A;Cross-references: EMBL:Z68218; PIDN: CAA92472.1; GSPDB: GN00022; CESP: K01H12.2
A;Experimental source: clone K01H12
C;Genetics:
A;Gene: CESP: K01H12.2
A;Map position: 4
A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.2%; Score 1043.5; DB 2; Length 313;
Best Local Similarity 69.4%; Pred. No. 8.5e-87;
Matches 202; Conservative 37; Mismatches 49; Indels 3; Gaps 2;
QY 8 FLKDFLAGAATAAASKTAVAPIERVKLLLOVQHASQKISAEKQYKGIIDCVVRIPEQ 67
DB 25 FLIDLASGGTAASVKTAVAPIERVKLLLOVQHASQKISAEKQYKGIIDCVVRIPEQ 84
QY 68 LSWFRGNLANVIRYPTQALNFAKDKYKQIFLGVDVRHKKQFWRYPAGNLASGGAAGA 127
DB 85 AALWRGNLANVIRYPTQALNFAKDKYKQIFLGVDVRHKKQFWRYPAGNLASGGAAGA 144
QY 128 LCFVYPLDFAARLAAVGRRA-OREPHGLGDCIIKIPKSDGLRGLVQGNVSVQGI 187
DB 145 LCFVYPLDFAARLAAVGRRA-OREPHGLGDCIIKIPKSDGLRGLVQGNVSVQGI 204
QY 188 AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPTDVRRRMMQSGRK 246
DB 205 AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPTDVRRRMMQSGRK 262
QY 247 DIMYTGTVDCWRKIADKQKAFKPGAWSNVLRGMGGAFLVLYDEIK 297
DB 263 DVLYKNTLDCVVKICKQSGGAFFKGAENLVRGTGGALVLYVYDEVK 313

RESULT 12

T25371
hypothetical protein T27E9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C;Accession: T25371
R;Lloyd, C.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z20024
A;Accession: T25371
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-300 <WIL>
A;Cross-references: EMBL:Z82059; PIDN: CAB04874.1; GSPDB: GN00021; CESP: T27E9.1
A;Experimental source: clone T27E9
C;Genetics:
A;Gene: CESP: T27E9.1
A;Map position: 3
A;Introns: 20/1; 41/3; 115/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 66.8%; Score 1037.5; DB 2; Length 300;
Best Local Similarity 69.1%; Pred. No. 2.8e-86;
Matches 201; Conservative 38; Mismatches 49; Indels 3; Gaps 2;

Db 68 QGVLSLWRGNVANVIRYFPTQAFNFAFYKQYFNIP-PRYDQNTDFSKFFCVNLSGATAG 126
QY 125 ATSLCFVYPLDFARTLAAADVGRRAQREPHGLGDCIIKIFKSDGLRGLYOGFNVSVQGI 184
Db 127 AISLLIYPLDFARTLADIGKGRQFTGLFDCLAKYKQTGLLSLYGGFVSVTGII 186
QY 185 IYRAAYFGVYDTAKGML-PDPKNVHIFVSMIAQSVTAVAGLLSYPPDTVRRMMMQSGR 243
Db 187 VYRGSYFGLYDSAKALLFTNDKNTNIVLKWAVAQSVTILAGLISYPPDTVRRMMMQSGR 246
QY 244 KG-ADIMYTGTVDCWRKIAKDEGAKAFKGANVLRGMGGAFVLVLYDEIKKYV 297
Db 247 KGKEIQYKNTIDCWIKILRNEGFKGFGAWANVIRGAGGALVLVYDELOKLI 301

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